

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.45573 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-11

Perfect score: 92
Sequence: 1 SGGTTVTVTLSDVNDNPP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	83	90.2	790	2	G02678 cadherin-14 - huma
2	83	90.2	793	2	D38992 cadherin 8 - huma
3	82	89.1	785	2	I50180 cadherin-7 - chick
4	81	88.0	790	2	I51638 F-cadherin - Afri
5	80	87.0	789	2	I52701 K-cadherin - rat
6	80	87.0	790	2	I50178 cadherin-6B - chic
7	80	87.0	790	2	I37016 cadherin-6 - huma
8	79	85.9	796	2	A38992 cadherin 11 precu
9	79	85.9	796	2	I48277 cadherin-11 - mous
10	79	85.9	796	2	I49556 cadherin-11 - mous
11	79	85.9	796	2	A53584 OB-cadherin precu
12	71	77.2	794	2	I59372 cadherin 12 - huma
13	67	72.8	780	2	T30213 G-cadherin - sea u
14	65	70.7	4351	2	T00252 MEGF1 protein - ra
15	62	67.4	784	1	IUHUC5 cadherin 5 precurs
16	62	67.4	877	1	IUBOCHN N-cadherin 2 precurs
17	62	67.4	906	1	IUHUCN cadherin 2 precurs
18	62	67.4	906	1	IUMSCN N-cadherin precurs
19	62	67.4	912	1	IUCHCN N-cadherin precurs
20	61	66.3	913	1	A47543 R-cadherin precurs
21	61	66.3	913	1	IUCHCR R-cadherin precurs
22	61	66.3	2610	2	T20968 hypothetical prote
23	58	63.0	4307	2	T20721 hypothetical prote
24	57	62.0	713	2	B38992 cadherin 13 precu
25	57	62.0	770	2	B48910 desmocollin 1b pre
26	57	62.0	824	2	A48910 desmocollin 1a pre
27	57	62.0	840	2	I37281 Desca precursor -
28	57	62.0	894	2	I37282 Descb precursor -
29	57	62.0	905	1	IUXLC1 N-cadherin 1 precu

30	57	62.0	906	1	IUXLC2 N-cadherin 2 precu
31	57	62.0	1715	2	JE0126 Bombyx mori recept
32	57	62.0	3097	2	T00021 DN-cadherin - frui
33	57	62.0	5147	1	IUFFTM cadherin-related t
34	56	60.9	373	2	T34563 hypothetical prote
35	56	60.9	882	1	IUHUCE BH-proc cadherin-a
36	56	60.9	1069	2	T00043 BH-proc cadherin p
37	56	60.9	1200	2	T00042 BH-proc cadherin p
38	56	60.9	1200	2	T00042 T-cadherin precurs
39	55	59.8	712	1	IUMSCT T-cadherin 2 - chi
40	55	59.8	717	2	I51206 desmocollin - bovl
41	55	59.8	896	2	I45858 seven-pass transme
42	55	59.8	3034	2	T14119 desmocollin, type
43	54	58.7	826	2	B53363 desmocollin, type
44	54	58.7	896	2	A53363 desmocollin, type
45	54	58.7	916	2	C38992 cadherin 4 precurs

ALIGNMENTS

RESULT 1

G02678
cadherin-14 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02678
R/Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A/Reference number: H01584
A/Accession: G02678
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <SH1>
A/Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AAH02933.1; PID:G13
C/Superfamily: cadherin; cadherin repeat homology <CDH>
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
DB 249 SGGTTVTVTLSDVNDNPP 266

RESULT 2

D38992
cadherin 8 - human
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MIMD:9128540; PMID:2059658
A/Accession: D38992
A/Molecule type: mRNA
A/Residues: 1-793 <SU2>
A/Cross-references: GB:I34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
C/Genetics:
A/Gene: GDB:CDH8
A/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 793;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 250 SGGTIVTVTLSDVNDNPP 267

RESULT 3

I50180
C:Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
R/Accession: I50180
R/Name: S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: I50178; MUID:95309115; PMID:7540531
A/Accession: I50180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NAK>
A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
F/156-267/Domain: cadherin repeat homology <CDH>

Query Match 89.1%; Score 82; DB 2; Length 785;
Best Local Similarity 83.3%; Pred. No. 7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 243 SGGTIVTVTLSDVNDNPP 260

RESULT 4

I51638
C:Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R/Accession: I51638; S55391
R/Name: A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A/Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: I51638; MUID:96039533; PMID:7496627
A/Accession: I51638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <ESP>
A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA59679.1; PID:98546
C/Suprafamily: cadherin; cadherin repeat homology
F/161-267/Domain: cadherin repeat homology <CR2>

Query Match 88.0%; Score 81; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 0.0001;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 248 AGTTVVNTLSDVNDNPP 265

RESULT 5

I52701
K-cadherin - rat
C:Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
R/Accession: I52701
R/Name: Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara,
Cancer Res. 54, 3034-3041, 1994
A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A/Reference number: I52701; MUID:94243827; PMID:8187093
A/Accession: I52701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RBS>

A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:943546
C/Genetics:
A/Gene: KCAD
C/Suprafamily: cadherin; cadherin repeat homology
F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 789;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 249 SGGTIVTVTLSDVNDNPP 266

RESULT 6

I50178
C:Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
R/Accession: I50178
R/Name: S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe
A/Reference number: I50178; MUID:95309115; PMID:7540531
A/Accession: I50178
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <NAK>
A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 249 SGGTIVTVTLSDVNDNPP 266

RESULT 7

I37016
C:Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
R/Accession: I37016
R/Name: Y.Y.; Gotlib, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the
A/Reference number: I37016; MUID:95262134; PMID:7743525
A/Accession: I37016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RBS>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:9974184; PIDN:BA06562.1; PID:997418
C/Genetics:
A/Gene: GDB:CDH6
A/Cross-references: GDB:5822908
C/Suprafamily: cadherin; cadherin repeat homology
F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
||:||||:||||:||||:
Db 249 SGGTIVTVTLSDVNDNPP 266

RESULT 8

A38992
 cadherin 11 precursor - human
 N/Alternate names: OB-cadherin, osteoblast
 C/Species: Homo sapiens (man)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: A38992
 R/Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous system
 A/Reference number: S24305; MUID:91283540; PMID:2059658
 A/Accession: A38992
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <SUZ>
 A/Cross-references: UNIPROT:P55287; GB:L34056; NID:G506403; PIDN:AAA35622.1; PID:G506404
 C/Genetics:
 A/Gene: GDB:CDH11; OB
 A/Cross-references: GDB:512891; OMIM:600023
 A/Map position: 16q22.1-16q22.1
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication
 F/56-159/Domain: cadherin repeat homology <CR1>
 F/162-268/Domain: cadherin repeat homology <CR2>
 F/1271-383/Domain: cadherin repeat homology <CR3>
 F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGGTATVTLSDVNDNPP 18
 ||:||||:|||||||
 Db 249 SGTATVTLTDVNDNPP 266

RESULT 9
 148277
 cadherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I48277
 R/Hofmann, I.; Balling, R.
 Dev. Biol. 169, 337-346, 1995
 A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
 A/Reference number: I48277; MUID:95269886; PMID:7750649
 A/Accession: I48277
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:G642796; PIDN:CAA54674.1; PID:96660
 C/Genetics:
 A/Gene: cad-11
 C/Superfamily: cadherin; cadherin repeat homology
 F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGGTATVTLSDVNDNPP 18
 ||:||||:|||||||
 Db 249 SGTATVTLTDVNDNPP 266

RESULT 10
 149556
 cadherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I49556
 R/Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head

A/Reference number: I49556; MUID:95269887; PMID:7750650
 A/Accession: I49556
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; GB:D31963; NID:G974190; PIDN:BAAB6730.1; PID:G974197
 F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGGTATVTLSDVNDNPP 18
 ||:||||:|||||||
 Db 249 SGTATVTLTDVNDNPP 266

RESULT 11
 A53584
 OB-cadherin precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A53584
 R/Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amann, B.
 J. Biol. Chem. 269, 12092-12098, 1994
 A/Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
 A/Reference number: A53584; MUID:94216322; PMID:8163513
 A/Accession: A53584
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-796 <OKA>
 A/Cross-references: UNIPROT:P55288; GB:D21253; NID:G994774; PIDN:BAAB4797.1; PID:G99477
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: transmembrane protein
 F/56-159/Domain: cadherin repeat homology <CR1>
 F/162-268/Domain: cadherin repeat homology <CR2>
 F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGGTATVTLSDVNDNPP 18
 ||:||||:|||||||
 Db 249 SGTATVTLTDVNDNPP 266

RESULT 12
 159372
 cadherin 12 - human
 N/Alternate names: Br-cadherin
 C/Species: Homo sapiens (man)
 C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C/Accession: I59372
 R/Selig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunzel, L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
 A/Title: Expressed cadherin pseudogenes are localized to the critical region of the spl
 A/Reference number: I59372; MUID:95249541; PMID:7731968
 A/Accession: I59372
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A/Molecule type: mRNA
 A/Residues: 1-794 <RES>
 A/Cross-references: UNIPROT:P55289; GB:L33477; NID:G793942; PIDN:AAAB48539.1; PID:G79394
 C/Genetics:
 A/Gene: GDB:CDH12
 A/Cross-references: GDB:596324
 A/Map position: 5p13-5p14
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
 F/162-269/Domain: cadherin repeat homology <CR1>
 F/162-269/Domain: cadherin repeat homology <CR2>
 F/1272-384/Domain: cadherin repeat homology <CR3>

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DS Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBL_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Brain;
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Oseki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isogai T., Sugano S.,
 RC -1- SUBMITTAL (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CL EMBL, AK057922; BAB71613.1; -
 DR HSSP; P12830; 1068.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0005509; Fcalcium ion binding; IEA.
 DR GO; GO:0007156; Pphomophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 4.
 KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;
 Query Match 100.0%; Score 92; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18
 DB 240 SGSTVTVTLSVDVNDNP 257
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=cdh24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBL_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Brain;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien L., Soares M.B., Bonaldo A., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosen S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Brain;
 RA Strausberg R.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002333; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;
 Query Match 100.0%; Score 92; DB 2; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18
 DB 240 SGSTVTVTLSVDVNDNP 257
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=cdh24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBL_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Brain;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien L., Soares M.B., Bonaldo A., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosen S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

```

RC      SEQUENCE FROM N.A.
RC STAIN=C57BL/6; TISSUE=Brain;
RA Straube R.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057373; AAH57373.1; -.
SQ      SEQUENCE      781 AA;  84104 MW;  15996D6EC9835AA CFC64;

Query Match      100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches      18; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      1  SGGTIVYVTLSDVNDNPP 18
DB      240  SGGTIVYVTLSDVNDNPP 257

RESULT 5
CADO_HUMAN
ID_CADO_HUMAN      STANDARD;      PRT;      819 AA.
AC      Q86F0; Q86UP; Q9N184;
DT      29-MAR-2004 (Rel. 43, Created)
DT      29-MAR-2004 (Rel. 43, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Cadherin-24 precursor (UNQ2834/PRO34009).
GN      Name=CDH24; Synonyms=CDH11L;
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
[1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP      CATENINS.
RX      MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA      Kafafi A.B., Nieman M.T., Wheelock M.U., Johnson K.R.;
RT      "Characterization of cadherin-24, a novel alternatively spliced type
RL      II cadherin.";
RL      J. Biol. Chem. 278:27513-27519(2003).
[2]
RN      SEQUENCE FROM N.A. (ISOFORM 2).
RP      MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RX      Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA      Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA      Eaton D., Foster J., Girmaldi C., Gu Q., Hase P.E., Heidens S.,
RA      Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA      Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA      Seshagiri S., Simone L., Singh J., Smith V., Stinson J., Vagts A.,
RA      Vanden R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,
RA      Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Zoddard A., Wood W.I.,
RA      Godowski P., Gray A.;
RT      "The secreted protein discovery initiative (SPDI), a large-scale
RT      effort to identify novel human secreted and transmembrane proteins: a
RT      bioinformatics assessment.";
RT      Genome Res. 13:2265-2270(2003).
[3]
RN      SEQUENCE FROM N.A. (ISOFORM 3).
RP      TISSUE=Testis;
RA      Blum H., Basterachs S., Mewe H.-W., Cassenhuber J., Wiemann S.;
RA      Submitted (JAN-2000) to the EMBL/GenBank/DBJ database.
[4]
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC      They preferentially interact with themselves in a homophilic
CC      manner in connecting cells; cadherins may thus contribute to the
CC      sorting of heterogeneous cell types. Cadherin-24 mediate strong
CC      cell-cell adhesion.
-1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
CC
-1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC
-1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1; Synonyms=Long form;
CC      IsoId=Q86UP0-1; Sequence=1displayed;
CC      Name=2; Synonyms=Short form;
CC      IsoId=Q86UP0-2; Sequence=VSP_008717;
CC      Name=3;

```

```
CC CC -1- SIMILARITY: Contains 5 cadherin domains.
CC Note=NO experimental confirmation available.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY260900; AAP20590.1; -.
DR EMBL; AY260901; AAP20591.1; -.
DR EMBL; AY358189; AA088566.1; -.
DR EMBL; AL151477; CAB0758.1; -.
DR PIR; T46418; T46418.
DR HSSP; P09803; I17W.
DR Genew; HGNC:14265; CDH24.
DR InterPro; IPRO00233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01043; Cadherin_C_1.
DR PRINTS; PR02005; CADHERIN.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS02068; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Multigene family; Repeat; Signal; Transmembrane.
FT SIGNAL 1 Potential.
FT PROPEP 21 44 Potential.
FT CHAIN 45 819 Cadherin_24.
FT DOMAIN 45 641 Extracellular (Potential).
FT TRANSMM 642 662 Potential.
FT DOMAIN 663 819 Cytoplasmic (Potential).
FT DOMAIN 46 150 Cadherin 1.
FT DOMAIN 151 259 Cadherin 2.
FT DOMAIN 260 374 Cadherin 3.
FT DOMAIN 375 517 Cadherin 4.
FT DOMAIN 517 630 Cadherin 5.
FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential).
FT CAROXYD 548 548 N-linked (GlcNAc...) (Potential).
FT CAROXYD 563 563 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 455 492 Missing (in isoform 2).
FT FT /FTId=VSP 008717.
FT FT MISSING (In isoform 3).
FT VARSPLIC 1 427 /FTId=VSP 008718.
FT FT EGTTITTAFLDEARAANNVTATLETGLSMGPDEGWPTLT
FT FT VAEMAPAAPQSRSEVGSAVLQD -> MNIVCTYCSHS
FT FT ATLFECTILHAYFMCFCLMELVASCGIHAAHPMLRVNCAVC
FT FT VMRVCFGVLPS (In isoform 3).
FT FT /FTId=VSP 008719.
SQ SEQUENCE 819 AA; 87751 MW; 9083034F18BA7E4A CRC64;
QY 1 SGGSTTVTLSDVNDNP 18
| | | | | | | | | | | | | | | | | | |
Db 240 SGSTTVTLSDVNDNP 257

RESULT 6
Q8BLB5 PRELIMINARY; PRT; 337 AA.
AC Q8BLB5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Mus musculus adult male corpora quadrigenina cDNA, RIKEN full-length
DE enriched library, clone:B230220E17 product:hypothetical cadherin
DE structure containing protein, full insert sequence. (fragment)
GN Name=B230220E17RIK;
OS Mus musculus(Mousee).
```


DR PRINTS; PR00205; CADHERIN.
 DR SWART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR DR PROSITE; PS00268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79149 MW; 5880598F638624A CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCSTTVTVTLSDVNDNP 18
 Db 257 SCSTTVTVTLSDVNDNP 274

RESULT 10
 Q8C449 PRELIMINARY; PRT; 716 AA.
 AC Q8C449;
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone: C630002D14 product: cadherin 8, full insert sequence
 DE (cdh8 protein).
 GN Name: Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT "The FANTOM Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN Integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Kato H., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bontad M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; BC057581; AAH57581.1; -;
 DR HSSP; P15116; INCU.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002326; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79145 MW; 976F5D845F9385D CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCSTTVTVTLSDVNDNP 18

```
DB 257 SGTTLVTTLVDVNDNP 274

RESULT 11
AAH57581 PRELIMINARY; PRT; 716 AA.
ID AAH57581;
AC AAH57581;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cdh8 protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hoplin R.F., Jordan H., Moore T., Vax S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
SQ EMBL: BC057581, AAH57581.1;
SQ SEQUENCE 716 AA; 79145 MW; 976FFSD845F938BD CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
Best Local Similarity 83.3%; Pred. No. 0.00026;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTLVTTLVDVNDNP 18
DB 257 SGTTLVTTLVDVNDNP 274

RESULT 12
Q5BRK4 PRELIMINARY; PRT; 754 AA.
ID Q5BRK4;
AC Q5BRK4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830035F13 product:cadherin 8, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kuno H., Akiyama J., Nishi K., Kikunai T., Teshiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishitani T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kawai H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda K., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira T., Takeeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK044046; BAC31751.1; -.
DR HSSP: P15116; INCU.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR000233; Cadherin.
DR InterPro: IPR002126; Cadherin.
DR Pfam: PF00028; Cadherin; 5.
DR PRINTS: PF01049; Cadherin; 1.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN 1; 3
```

DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;

Query Match
 Best Local Similarity 83.3%; Score 83; DB 2; Length 754;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNP 18
 |||:||||:|||||
 Db 257 SGTTTLVTLVDNDNP 274

RESULT 13
 CADI_HUMAN STANDARD; PRT; 790 AA.
 ID CADI_HUMAN
 AC Q13634;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-18 precursor (cadherin-14).
 GN Name=CDH18; Synonyms=CDH14;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184182; PubMed=9030594;
 RA Shibata T., Shimoyama Y., Gotch M., Hirohashi S.;
 RT "Identification of human cadherin-14, a novel neurally specific type,
 RT II cadherin, by protein interaction cloning";
 RL J. Biol. Chem. 272:5236-5240(1997).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U59325; AAB02933.1; -
 DR PIR; G02678; G02678.
 DR HSSP; P09803; 117X.
 DR Genew; HGNC:1757; CDH18.
 DR MIM; 603019; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 790 Cadherin-18.
 FT DOMAIN 54 608 Extracellular (Potential).
 FT TRANSMEM 609 636 Potential.
 FT DOMAIN 637 790 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.

FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 790 AA; 88072 MW; 5C7BDEB229B6EDCA CRC64;

Query Match
 Best Local Similarity 90.2%; Score 83; DB 1; Length 790;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNP 18
 |||:||||:|||||
 Db 249 SGSTVTVTLVDNDNP 266

RESULT 14
 CADH_HUMAN STANDARD; PRT; 799 AA.
 ID CADH_HUMAN
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=10861224;
 RX Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
 RA "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins";
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Heilmann R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue";
 RL Cell Regul. 2:261-270(1991).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC


```

DR EMBL: AB035305; BAAB7419.1; -.
DR EMBL: U34060; AA35628.1; ALT_INIT.
DR HSSP: P09803; 117W.
DR Genew: HGNC:1767; CDH8.
DR MIM: 603008; -.
DR GO: GO:0007155; P:cell adhesion; TAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
  Transmembrane.
KM SIGNAL 1 29 Potential.
  PROPEP 30 61 Potential.
  CHAIN 62 799 Cadherin-8.
  DOMAIN 62 621 Extracellular (Potential).
  TRANSMEM 622 642 Potential.
  DOMAIN 643 799 Cytoplasmic (Potential).
  DOMAIN 643 799 Cadherin 1.
  DOMAIN 168 276 Cadherin 2.
  DOMAIN 277 391 Cadherin 3.
  DOMAIN 392 494 Cadherin 4.
  DOMAIN 495 616 Cadherin 5.
  CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
  CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
  CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
  CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
  CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
  CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
  CONFLICT 355 355 V -> D (in Ref. 2 and 3).
  CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
SQ SEQUENCE 799 AA; 88253 MW; 9B1198B6039C6A0A CRC64;

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNP 18
DB 257 SGTTLTTLTDVNDNP 274

RESULT 15
CAD8-MOUSE STANDARD; FRT; 799 AA.
AC 297251;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-8 precursor.
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=97174321; Pubmed=9022055;
RA Korematsu K., Redies C.;
RT "Restricted expression of cadherin-8 in segmental and functional
  subdivisions of the embryonic mouse brain.";
RL Dev. Dyn. 208:178-189(1997).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
  They preferentially interact with themselves in a homophilic
  manner in connecting cells; cadherins may thus contribute to the
  sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 5 cadherin domains.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X95600; CA64857.1; -.
DR HSSP: P09803; 117W.
DR MGD: MG1:107434; Cdh8.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
  Transmembrane.
KM SIGNAL 1 29 Potential.
  PROPEP 30 61 Potential.
  CHAIN 62 799 Extracellular (Potential).
  DOMAIN 62 621 Cytoplasmic (Potential).
  TRANSMEM 622 642 Potential.
  DOMAIN 643 799 Cadherin 1.
  DOMAIN 168 276 Cadherin 2.
  DOMAIN 277 391 Cadherin 3.
  DOMAIN 392 494 Cadherin 4.
  DOMAIN 495 616 Cadherin 5.
  CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
  CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
  CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
  CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
  CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
  CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNP 18
DB 257 SGTTLTTLTDVNDNP 274

```

Search completed: December 8, 2004, 10:24:39
 Job time : 8.21488 secs

This Page Blank (uspto)

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancer, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA:

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNP 18
DB 1 SGGTIVTVTLSDVNDNP 18

RESULT 2

ADD29452
ID ADD29452 standard; peptide; 18 AA.

AC ADD29452;
XX
DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein peptide fragment Seq ID11.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour, human.

OS Homo sapiens.

XX
PN US200314491-A1.

PD 31-JUL-2003.

XX
PF 16-FEB-2001; 2001US-00786051.

XX
PR 03-FEB-2000; 2000US-00436914.
PR 27-APR-2000; 2000US-00560875.

PA (GDB/) GDBOLE S D.

PA (KLOC/) KIO C.

PA (ARTE/) ARTERBURN M C.

PA (YERN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LUC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancer, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 11; 63pp; English.

CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancer, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA:

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNP 18
DB 1 SGGTIVTVTLSDVNDNP 18

RESULT 3

AD116946
ID AD116946 standard; protein; 493 AA.

AC AD116946;
XX

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SegID 482.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

XX inflammation; autoimmune disorder; allergy; blood disorder;

XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;

XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;

XX Alzheimer's disease; infection; str.

OS Homo sapiens.

XX
PN WO200268649-A2.

PD 06-SEP-2002.

XX
PF 31-JAN-2002; 2002WO-US002785.

XX
PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 31-JAN-2001; 2001US-0265517P.

PR 02-FEB-2001; 2001US-0266406P.

PR 05-FEB-2001; 2001US-0266975P.

PR 07-FEB-2001; 2001US-0267057P.

PR 08-FEB-2001; 2001US-0267453P.

PR 09-FEB-2001; 2001US-0267823P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 27-FEB-2001; 2001US-0271855P.

PR 02-MAR-2001; 2001US-0272788P.

PR 14-MAR-2001; 2001US-0275252P.

PR 14-MAR-2001; 2001US-0275947P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282929P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285123P.
 PR 23-APR-2001; 2001US-0285743P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312689P.
 PR 16-AUG-2001; 2001US-0313908P.
 PR 21-AUG-2001; 2001US-0313909P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0315447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 12-SEP-2001; 2001US-0318118P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

PI Tcheney VT, Spylex KA, Zernhusen BD, Paturaian M, Shinkets RA;
 PI Li L, Gargolli BA, Padigar M, Anderson DM, Rastelli L, Miller CE;
 PI Getlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CEA;
 PI Furrak K, Grosse WM, Alsdbrook JF, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2002-706998/76.

PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, or
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Disclosure; SEQ ID NO 482; 1498bp; English.

CC This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, cardiant, antiinflammatory, immunosuppressive, anti-allergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC haemostatic, nephrotropic, antirheumatic, hepatotropic,
 CC neuroprotective, noctropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.

XX Sequence 493 AA;

Query Match

100.0%; Score 92; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. No. 5.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTVTVTLSDVNDNP 18
 Db 240 SGGSTVTVTLSDVNDNP 257

RESULT 4
 ABB53295
 ID ABB53295 standard; protein; 607 AA.

XX ABB53295;
 AC ABB53295;
 DT 12-FEB-2002 (first entry)

XX Human polypeptide #35.

XX Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic;
 KW antiinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;
 KW nephrotropic; anorectic; cytosstatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199633P.

XX 11-MAY-2000; 2000US-0203386P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kohnick KS;
 PI Lal Y, Xie Q;
 XX WPI; 2002-041392/05.

XX N-PSDB; ABA90360.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

XX Claim 1; Page 106-108; 116bp; English.

CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, parasympathetic palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 XX
 SQ Sequence 607 AA;

Query Match 100.0%; Score 92; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSDVNDNPP 18
 |||||
 DB 240 SGGSTVTVTLSDVNDNPP 257

RESULT 5

ADD29448
 ID ADD29448 standard; protein; 620 AA.

AC ADD29448;
 XX

DT 15-JAN-2004 (first entry)
 XX

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
 KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 XX metastatic tumour; human.

OS Homo sapiens.

PN US200314491-A1.

PD 31-JUL-2003.

PE 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LITC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 7; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutic useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the
 CC invention.
 XX
 SQ Sequence 620 AA;

Query Match 100.0%; Score 92; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSDVNDNPP 18
 |||||
 DB 224 SGGSTVTVTLSDVNDNPP 241

RESULT 6

ADD29445
 ID ADD29445 standard; protein; 636 AA.

AC ADD29445;
 XX

DT 15-JAN-2004 (first entry)
 XX

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
 KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 XX metastatic tumour; human.

OS Homo sapiens.

PN US200314491-A1.

PD 31-JUL-2003.

PE 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LITC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 4; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may

allow development of therapeutics useful for the treatment of diseases
such as cancers, osteoporosis, Paget's disease, osteomalacia,
hyperostosis and osteopetrosis. The protein and DNA sequence of the
invention may also be useful as markers for prognosis of metastatic
tumours. The present sequence is that of the human secreted cadherin-like
protein of the invention.

Sequence 636 AA;

Query Match 100.0%; Score 92; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTYVTLSDVNDNPP 18
DB 240 SGGTTVTYVTLSDVNDNPP 257

RESULT 7
ABBS3296
ID ABB53296 standard; protein; 781 AA.

AC ABB53296;
XX
DT 12-FEB-2002 (first entry)

XX Human polypeptide #36.

XX Human; nocitropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic;
XX antiinflammatory; antilipemic; hepatotropic; vincicide; antidiabetic;
XX nephrotropic; anorectic; cyrostatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-0203336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Agatwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;

XX Lai Y, Xie Q;

XX WPI; 2002-041392/05.

XX N-PSDB; ABA90361.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 844, 782, 622, 394, 471, 485, 286, 513, 495, 350, 619, 490, 462, 285,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including
XX Alzheimer's, paraspinal nerve palsy, Huntington's disease, myotonic
XX dystrophy, anorexia and depression; cardiovascular diseases including

congestive heart failure, Hodgkin's disease and myocardial infarction;
respiratory diseases including asthma, chronic obstructive pulmonary
disease, cystic fibrosis and adult respiratory distress syndrome; liver
diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
renal disease including renal failure, acute tubular necrosis and
glomerulonephritis; skeletal muscle diseases including Ehlerburg's
disease, hypoglycaemia and obesity; gastrointestinal diseases including
myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
of testes including testicular cancer, male reproductive diseases
including low testosterone and male infertility; and disease of pancreas
including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
present sequence is a polypeptide of the invention

Sequence 781 AA;

Query Match 100.0%; Score 92; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTYVTLSDVNDNPP 18
DB 240 SGGTTVTYVTLSDVNDNPP 257

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

XX 28-MAR-2002 (first entry)

XX Human cadherin family member 57805, protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarrhythmic; antineuritic;
XX dermatological; immunosuppressive; antiinflammatory; antipsoriatic;
XX antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
XX antihypertic; hypotensive; antiarteriosclerotic; cardiant; antiarrhythmic;
XX anorectic; immunomodulatory; vasotropic; vincicide; cyrostatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016013.

XX 19-MAY-2000; 2000US-0205674P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RM;

XX WPI; 2002-083082/11.

XX N-PSDB; ABA96406, ABA96407.

XX The invention relates to human cadherin family polypeptide designated
XX Claim 9, Page 105, 11pp; English.
XX New human cadherin family protein and polynucleotides, useful for
XX diagnosing and treating disorders e.g. obstructive jaundice, multiple
XX sclerosis, encephalomyelitis and atherosclerosis and to identify
XX modulators of therapeutic use.

CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarrhythmic, antirheumatic, dermatological,
 CC immunosuppressive, antineoplastic, antiparasitic, antisthmatic,
 CC anti-allergic, antileptotic, haemostatic, antipruritic, anticholinergic,
 CC hypotensive, antiserotoclastic, cardiac, antirhythmic, anorectic,
 CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy, cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis, viral diseases, metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

CC SQ Sequence 781 AA;

QY Query Match 100.0%; Score 92; DB 5; Length 781;
 DB Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGGTTVTVTLSDVNDNPP 18
 |||||
 240 SGGTTVTVTLSDVNDNPP 257

RESULT 9
 ABG34078
 ID ABG34078 standard; protein; 781 AA.
 XX
 AC ABG34078;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human Pro peptide #49.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KM tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 EN WO200224888-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US027099.
 XX
 PR 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0264421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001US-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GENT) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gunney AL, Smith V, Stephan U, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 XX WPI; 2002-362426/39.
 DR N-PSDB; ABK70009.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX
 PS Claim 11; Fig 98; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. Polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention

CC SQ Sequence 781 AA;

QY Query Match 100.0%; Score 92; DB 5; Length 781;
 DB Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGGTTVTVTLSDVNDNPP 18
 |||||
 240 SGGTTVTVTLSDVNDNPP 257

RESULT 10
 AD116604
 ID AD116604 standard; protein; 781 AA.
 XX
 AC AD116604;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human NOVX protein to treat human pathological conditions Segid140.
 XX
 KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytostatic; cardiac; anti-inflammatory; immunosuppressive; anti-allergic;
 KW haemostatic; anti-HIV; antidiabetic; antiserotoclastic; anorectic;
 KW antiaesthetic; nephrotropic; antiarrhythmic; hepatotropic;
 KW neuroprotective; neoprotic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.

XX	OS	Homio sapiens.
XX	PN	WO200268649-A2.
XX	PD	06-SEP-2002.
XX	PF	31-JAN-2002; 2002WO-US002785.
XX	PR	31-JAN-2001; 2001US-0265395P.
XX	PR	31-JAN-2001; 2001US-0265412P.
XX	PR	31-JAN-2001; 2001US-0265514P.
XX	PR	31-JAN-2001; 2001US-0265517P.
XX	PR	02-FEB-2001; 2001US-0266406P.
XX	PR	05-FEB-2001; 2001US-0266767P.
XX	PR	07-FEB-2001; 2001US-0266875P.
XX	PR	07-FEB-2001; 2001US-0267057P.
XX	PR	08-FEB-2001; 2001US-0267459P.
XX	PR	09-FEB-2001; 2001US-0267823P.
XX	PR	15-FEB-2001; 2001US-0268974P.
XX	PR	26-FEB-2001; 2001US-0271664P.
XX	PR	27-FEB-2001; 2001US-0271839P.
XX	PR	27-FEB-2001; 2001US-0271855P.
XX	PR	02-MAR-2001; 2001US-0272788P.
XX	PR	02-MAR-2001; 2001US-0273046P.
XX	PR	14-MAR-2001; 2001US-0275925P.
XX	PR	14-MAR-2001; 2001US-0275947P.
XX	PR	14-MAR-2001; 2001US-0275950P.
XX	PR	14-MAR-2001; 2001US-0275959P.
XX	PR	15-MAR-2001; 2001US-0276448P.
XX	PR	15-MAR-2001; 2001US-0276450P.
XX	PR	16-MAR-2001; 2001US-0276397P.
XX	PR	16-MAR-2001; 2001US-0276768P.
XX	PR	20-MAR-2001; 2001US-0278652P.
XX	PR	26-MAR-2001; 2001US-0278775P.
XX	PR	26-MAR-2001; 2001US-0278778P.
XX	PR	29-MAR-2001; 2001US-0279882P.
XX	PR	29-MAR-2001; 2001US-0279884P.
XX	PR	30-MAR-2001; 2001US-0280147P.
XX	PR	11-APR-2001; 2001US-0282992P.
XX	PR	11-APR-2001; 2001US-0283083P.
XX	PR	20-APR-2001; 2001US-0285133P.
XX	PR	23-APR-2001; 2001US-0285749P.
XX	PR	03-MAY-2001; 2001US-0288327P.
XX	PR	03-MAY-2001; 2001US-0288504P.
XX	PR	29-MAY-2001; 2001US-0294047P.
XX	PR	30-MAY-2001; 2001US-0294473P.
XX	PR	08-JUN-2001; 2001US-0296964P.
XX	PR	18-JUN-2001; 2001US-0298959P.
XX	PR	19-JUN-2001; 2001US-0299334P.
XX	PR	13-AUG-2001; 2001US-0312020P.
XX	PR	16-AUG-2001; 2001US-0312889P.
XX	PR	16-AUG-2001; 2001US-0312908P.
XX	PR	21-AUG-2001; 2001US-0313390P.
XX	PR	28-AUG-2001; 2001US-0315470P.
XX	PR	31-AUG-2001; 2001US-0316447P.
XX	PR	07-SEP-2001; 2001US-0318115P.
XX	PR	07-SEP-2001; 2001US-0318118P.
XX	PR	12-SEP-2001; 2001US-0318740P.
XX	PR	19-SEP-2001; 2001US-0333379P.
XX	PR	18-OCT-2001; 2001US-0330245P.
XX	PR	18-OCT-2001; 2001US-0330308P.
XX	PR	14-NOV-2001; 2001US-0332701P.
XX	PR	(CURA-) CURAGEN CORP.
XX	PI	Tcharenev VT, Spytek KA, Zernhusen BD, Patturajan M, Shinkets RA,
XX	PI	Li L, Gangolli EA, Pedigaru M, Anderson DW, Rastelli L, Miller CE;
XX	PI	Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA,
XX	PI	Futrek K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE,
XX	PI	WPI: 2002-706998/76.
XX	PI	INDIA INDIA6603.

XX	New NOXV polypeptides and nucleic acids, useful for preventing or
PT	treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
PT	atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT	pharmacogenomics.
XX	
XX	Claim 1; SEQ ID NO 140; 1498bp; English.
XX	
CC	This invention relates to a novel nucleic acids, and encoded polypeptides
CC	thereof, which have properties related to the stimulation of biochemical
CC	or physiological responses in a cell, tissue, organ or organism.
CC	Specifically, it refers to the use of biologically active fragments for
CC	diagnostic and prognostic assays and furthermore in the treatment of
CC	diverse pathological conditions. The present invention describes novel
CC	human and murine NOXV proteins, as well as methods to modulate their
CC	expression using antisense oligos, ribozymes and peptide nucleic acids.
CC	The NOXV polypeptides, polymucleotides and antibodies are useful in
CC	treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
CC	atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC	treatment or preventing diseases such as inflammation, autoimmune
CC	disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC	(AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC	arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC	and epilepsy. Accordingly, these molecules have many activities including
CC	cytostatic, cardiant, anti-inflammatory, immunosuppressive, antiallergic,
CC	haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC	antiasmatic, nephrotropic, antiarthritic, hepatotropic,
CC	neuroprotective, nootropic, antibacterial, virocidic, antiparasitic,
CC	relaxant and anticoincitant. In addition, they are useful in screening
CC	assays to identify small molecules that modulate or inhibit, for example,
CC	neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC	used as in chromosome mapping, tissue typing, preventive medicine and
CC	pharmacogenomics. This polypeptide is a human NOXV protein of the
CC	invention.
XX	
SQ	Sequence 761 AA:
Query Match	100.0%; Score 92; DB 5; Length 761;
Best Local Similarity	100.0%; P-rod. No. 9.5e-06;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 SGGTTVTTLSDVNDNPP 18
Dd	240 SGGTTVTTLSDVNDNPP 257
RESULT 11	
AD116606	
ID	AD116606 standard; protein; 761 AA.
XX	
AC	AD116606;
XX	
TU	15-APR-2004 (first entry)
DE	
XX	Human NOXV protein to treat human pathological conditions SeqID142.
XX	
KM	human; NOXV; cardiomyopathy; atherosclerosis; cancer; diabetes;
KM	inflammation; autoimmune disorder; allergy; blood disorder;
KM	acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KM	immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
KM	Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KM	cytostatic; cardiant; anti-inflammatory; immunosuppressive; antiallergic;
KM	haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KM	antiasmatic; nephrotropic; antiarthritic; hepatotropic;
KM	neuroprotective; nootropic; antibacterial; virocidic; antiparasitic;
KM	relaxant; anticoincitant; neurogenesis; wound healing; angiogenesis;
KM	chromosome mapping; tissue typing; pharmacogenomic.
OS	Homo sapiens.
XX	
PN	WO200268649-A2.
XX	
PD	06-SEP-2002.

PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCYTE GENOMICS INC.)
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TM, Yue H,
XX Forsythe JD, Elliott VS, Griffith JA, Gorvad AE, Azimtai Y,
XX Kallik DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S,
XX Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J,
XX WPI: 2003-354645/33.
XX N-PSDB; ACC00402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
XX useful for diagnosing, treating or preventing disorders associated with
XX aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX or stroke.
XX
XX Claim 1; Page 192-194; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis).
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTTVTLSDVNDNPP 18
DB 240 SGGSTTVTLSDVNDNPP 257
RESULT 13
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
XX ADA01366;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human PRO polypeptide #49.
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteoporosis; antirheumatic; antiarthritic.
XX
XX Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX

XX (SETH) GENENTECH INC.
XX Baker KP, Eaton DU, Filvaroff E, Goddard A, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
XX Fong S;
XX
XX WPI: 2003-625484/59.
XX N-PSDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polypeptide of the invention.
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTTVTLSDVNDNPP 18
DB 240 SGGSTTVTLSDVNDNPP 257
RESULT 14
ADA43795
ID ADA43795 standard; protein; 781 AA.
XX
XX ADA43795;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO34009.
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX microvascular endothelial cell tube formation; chondrocyte cell differentiation;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX US2003064474-A1.
XX
XX 03-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245859.
XX

KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 OS Homo sapiens.
 PN US2003073196-A1.
 XX
 XX
 PD 17-APR-2003.
 XX
 XX
 PF 18-SEP-2002; 2002US-00246210.
 XX
 XX
 PR 04-APR-2001; 2001US-0282199P.
 PR 23-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 PA (GENH) GENENTECH INC.
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gunney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 DR WPI; 2003-743814/70.
 DR N-PSDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO2183 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 XX
 PS Claim 11; Fig 98; 307P; English.
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide, an extracellular domain of PRO
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agant) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO2183 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 CC
 SQ Sequence 781 AA;
 XX
 XX
 Query Match 100.0%; Score 92; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9, 5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Dec 8 11:46:20 2004

us-09-788-051-11.rag

Page 11

Db 240 SGSTTVTLSDVNDNPP 257

Search completed: December 8, 2004, 10:13:06
Job time : 8.44864 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 18.3932 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-11
Perfect score: 92
Sequence: 1 SGSTTVTLSDVNDNPP 18

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	92	100.0	18	US-09-788-051-11
2	92	100.0	18	US-09-788-051-12
3	92	100.0	493	US-10-072-012-482
4	92	100.0	607	US-10-258-951-74
5	92	100.0	620	US-09-788-051-7
6	92	100.0	636	US-09-788-051-4
7	92	100.0	781	US-09-860-868-2
8	92	100.0	781	US-10-245-752-98
9	92	100.0	781	US-10-245-859-98
10	92	100.0	781	US-10-245-103-98
11	92	100.0	781	US-10-245-107-98
12	92	100.0	781	US-10-245-143-98
13	92	100.0	781	US-10-245-771-98

14	92	100.0	781	US-10-245-851-98	Sequence 98, Appl
15	92	100.0	781	US-10-245-883-98	Sequence 98, Appl
16	92	100.0	781	US-10-237-535-98	Sequence 98, Appl
17	92	100.0	781	US-10-238-183-98	Sequence 98, Appl
18	92	100.0	781	US-10-238-283-98	Sequence 98, Appl
19	92	100.0	781	US-10-238-370-98	Sequence 98, Appl
20	92	100.0	781	US-10-245-055-98	Sequence 98, Appl
21	92	100.0	781	US-10-245-147-98	Sequence 98, Appl
22	92	100.0	781	US-10-245-730-98	Sequence 98, Appl
23	92	100.0	781	US-10-245-739-98	Sequence 98, Appl
24	92	100.0	781	US-10-246-210-98	Sequence 98, Appl
25	92	100.0	781	US-10-239-196-98	Sequence 98, Appl
26	92	100.0	781	US-10-243-024-98	Sequence 98, Appl
27	92	100.0	781	US-10-243-409-98	Sequence 98, Appl
28	92	100.0	781	US-10-245-621-98	Sequence 98, Appl
29	92	100.0	781	US-10-245-880-98	Sequence 98, Appl
30	92	100.0	781	US-10-245-033-98	Sequence 98, Appl
31	92	100.0	781	US-10-243-095-98	Sequence 98, Appl
32	92	100.0	781	US-10-245-185-98	Sequence 98, Appl
33	92	100.0	781	US-10-245-427-98	Sequence 98, Appl
34	92	100.0	781	US-10-245-473-98	Sequence 98, Appl
35	92	100.0	781	US-10-245-770-98	Sequence 98, Appl
36	92	100.0	781	US-10-245-877-98	Sequence 98, Appl
37	92	100.0	781	US-10-246-976-98	Sequence 98, Appl
38	92	100.0	781	US-10-243-340-98	Sequence 98, Appl
39	92	100.0	781	US-10-162-435-13	Sequence 13, Appl
40	92	100.0	781	US-10-242-743-98	Sequence 98, Appl
41	92	100.0	781	US-10-242-845-98	Sequence 98, Appl
42	92	100.0	781	US-10-237-636-98	Sequence 98, Appl
43	92	100.0	781	US-10-238-325-98	Sequence 98, Appl
44	92	100.0	781	US-10-238-346-98	Sequence 98, Appl
45	92	100.0	781	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-11
Sequence 11, Application US/09788051
Publication No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimaec, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-11

Query Match 100.0%; Score 92; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGSTTVTLSDVNDNPP 18

Db 1 SGSTTVTTLSDVNDNP 18

RESULT 2

US-09-788-051-12
Sequence 12, Application US/09788051
Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chia-Yun
APPLICANT: Atreburu, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
POLYNUCLEOTIDES
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788, 051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-12

Query Match

Best Local Similarity 100.0%; Score 92; DB 10; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTTVTTLSDVNDNP 18

Db 1 SGSTTVTTLSDVNDNP 18

RESULT 3

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar
APPLICANT: Seytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkels, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

Db 1 SGSTTVTTLSDVNDNP 18

RESULT 4

US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kahnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258, 951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match

Best Local Similarity 100.0%; Score 92; DB 15; Length 493;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTTVTTLSDVNDNP 18

Db 240 SGSTTVTTLSDVNDNP 257

Query Match 100.0%; Score 92; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimaec, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 92; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 224 SGGTTVTTLSDVNDNP 241

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimaec, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.0

; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 92; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-868-2

Query Match 100.0%; Score 92; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

```
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-752-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTTVTVTLSDVNDNPP 18
Db      240  SGGTTVTVTLSDVNDNPP 257

RESULT 9
US-10-245-859-98
/ Sequence 98, Application US/10245859
/ Publication No. US20030064474A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
```

```
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-859-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTTVTVTLSDVNDNPP 18
Db      240  SGGTTVTVTLSDVNDNPP 257

RESULT 10
US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US20030068778A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C112
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTTVTVTLSDVNDNPP 18
Db      240  SGGTTVTVTLSDVNDNPP 257
```

Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 11

US-10-245-107-98

Sequence 98, Application US/10245107

Publication No. US2003006879A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watambe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C71

CURRENT APPLICATION NUMBER: US/10/245,107

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-107-98

Query Match 100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNP 18

Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 12

US-10-245-143-98

Sequence 98, Application US/10245143

Publication No. US2003006878A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C98

CURRENT APPLICATION NUMBER: US/10/245,143

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watambe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C90

CURRENT APPLICATION NUMBER: US/10/245,143

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNP 18

Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 13

US-10-245-771-98

Sequence 98, Application US/10245771

Publication No. US2003006878A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watambe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C98

CURRENT APPLICATION NUMBER: US/10/245,771

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTYTLSPVNDNPP 18
Db 240 SGGTWTYTLSPVNDNPP 257

RESULT 14
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC93
; CURRENT APPLICATION NUMBER: US/10/245, 851
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTYTLSPVNDNPP 18
Db 240 SGGTWTYTLSPVNDNPP 257

RESULT 15
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTYTLSPVNDNPP 18
Db 240 SGGTWTYTLSPVNDNPP 257

RESULT 15
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Wed Dec 8 11:46:20 2004

us-09-788-051-11.rapb

Page 7

Cy 1 SGSTTVTLSDVNDNPP 18
| | | | | | | | | |
Db 240 SGSTTVTLSDVNDNPP 257

Search completed: December 8, 2004, 11:34:29
Job time : 18.3932 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 2.1464 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-11

Perfect score: 92

Sequence: 1 SGSTVTWTLSDVNDNPP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	90.2	109	3	US-09-187-859-17
2	83	90.2	109	4	US-09-839-542B-17
3	83	90.2	109	4	US-09-535-852-17
4	83	90.2	532	1	US-08-188-228-44
5	83	90.2	532	1	US-08-332-638-44
6	83	90.2	793	1	US-08-188-228-54
7	83	90.2	793	1	US-08-332-643-48
8	83	90.2	793	1	US-08-332-638-54
9	83	90.2	799	1	US-08-188-228-42
10	83	90.2	799	1	US-08-332-638-42
11	82	89.1	109	4	US-09-187-859-11
12	82	89.1	109	4	US-09-839-542B-11
13	82	89.1	109	4	US-09-535-852-11
14	80	87.0	109	3	US-09-187-859-8
15	80	87.0	109	4	US-09-187-859-23
16	80	87.0	109	4	US-09-839-542B-8
17	80	87.0	109	4	US-09-839-542B-23
18	80	87.0	109	4	US-09-535-852-8
19	80	87.0	109	4	US-09-535-852-23
20	80	87.0	653	1	US-08-188-228-46
21	80	87.0	653	1	US-08-332-638-46
22	79	85.9	109	3	US-09-187-859-5
23	79	85.9	109	3	US-09-839-542B-5
24	79	85.9	109	4	US-09-535-852-5
25	79	85.9	635	2	US-08-738-349-12
26	79	85.9	635	2	US-08-738-349-6
27	79	85.9	693	4	US-09-919-497-55

28	79	85.9	796	1	US-08-188-228-58	Sequence 58, Appl
29	79	85.9	796	1	US-08-332-643-52	Sequence 52, Appl
30	79	85.9	796	1	US-08-332-638-58	Sequence 58, Appl
31	79	85.9	796	2	US-08-738-349-2	Sequence 2, Appl
32	79	85.9	796	2	US-08-738-349-4	Sequence 4, Appl
33	79	85.9	796	4	US-09-654-328-2	Sequence 15, Appl
34	71	77.2	109	3	US-09-187-859-15	Sequence 15, Appl
35	71	77.2	109	4	US-09-839-542B-15	Sequence 15, Appl
36	71	77.2	109	4	US-09-535-852-15	Sequence 15, Appl
37	71	77.2	794	1	US-08-188-228-60	Sequence 60, Appl
38	71	77.2	794	1	US-08-332-643-54	Sequence 54, Appl
39	71	77.2	794	1	US-08-332-638-60	Sequence 60, Appl
40	62	67.4	148	1	US-07-998-003A-36	Sequence 36, Appl
41	62	67.4	148	1	US-08-453-274B-36	Sequence 36, Appl
42	62	67.4	148	1	US-08-453-695A-36	Sequence 36, Appl
43	62	67.4	148	1	US-08-268-161A-36	Sequence 36, Appl
44	62	67.4	148	2	US-08-453-702A-36	Sequence 36, Appl
45	62	67.4	148	3	US-09-099-639-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-187-859-17
Sequence 17, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-17

Query Match 90.2% Score 83; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTVTWTLSDVNDNPP 18
DB 90 SGSTVTWTLSDVNDNPP 107

RESULT 2
US-09-839-542B-17
Sequence 17, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-839-542B-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 90 SGGTWTVTLSVDNDNP 107

RESULT 3
US-09-535-852-17
; Sequence 17, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.4076
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 90 SGGTWTVTLSVDNDNP 107

RESULT 4
US-08-188-228-44
; Sequence 44, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 257 SGGTWTVTLSVDNDNP 274

RESULT 5
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18

Wed Dec 8 11:46:20 2004

us-09-788-051-11.ra1

Page 3

Db 257 SGTTLVTLTDVNDNP 274

RESULT 6

US-08-188-228-54

Sequence 54, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5697725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-188-228-54

QY 1 SGTTLVTLTDVNDNP 18

Db 250 SGTTLVTLTDVNDNP 267

RESULT 7

US-08-332-643-48

Sequence 48, Application US/08332643

Patent No. 5638634

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Two First National Plaza, 20 South Clark

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/872,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

QY 1 SGTTLVTLTDVNDNP 18

Db 250 SGTTLVTLTDVNDNP 267

RESULT 8

US-08-332-638-54

Sequence 54, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVLTSDVNDNP 18
Db 250 SGTITLVTLTDVNDNP 267

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19-APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVLTSDVNDNP 18
Db 257 SGTITLVTLTDVNDNP 274

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVLTSDVNDNP 18
Db 257 SGTITLVTLTDVNDNP 274

RESULT 11
US-09-187-859-11
Sequence 11, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-187-859-11

Query Match 89.1%; Score 82; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTISVTITLDVNDNPP 107

RESULT 12
US-09-839-542B-11
Sequence 11, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-839-542B-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTISVTITLDVNDNPP 107

RESULT 13
US-09-535-852-11
Sequence 11, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-535-852-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18

DB 90 SGTISVTITLDVNDNPP 107

RESULT 14
US-09-187-859-8
Sequence 8, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-8

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTIVNITITLDVNDNPP 107

RESULT 15
US-09-187-859-23
Sequence 23, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 109
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-187-859-23

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTIVNITITLDVNDNPP 107

Search completed: December 8, 2004, 10:01:13
Job time : 2.1464 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.45573 Seconds

(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-12

Perfect score: 92

Sequence: 1 SGSTVTVTLSVDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	90.2	790	2 G02678	cadherin-14 - huma
2	83	90.2	793	2 D38992	cadherin 8 - huma
3	82	89.1	785	2 I50180	cadherin-7 - chick
4	81	88.0	790	2 I51638	F-cadherin - Affic
5	80	87.0	789	2 I52701	K-cadherin - rat
6	80	87.0	790	2 I50178	cadherin-6B - chic
7	80	87.0	790	2 I37015	cadherin-6 - huma
8	79	85.9	796	2 A38892	cadherin 11 precu
9	79	85.9	796	2 I48277	cadherin-11 - mous
10	79	85.9	796	2 I49556	OB-cadherin-12 - huma
11	79	85.9	796	2 A53584	cadherin 12 - huma
12	71	77.2	794	2 I59372	cadherin-12 - huma
13	67	72.8	2809	2 T30213	MEG1 protein - ra
14	65	70.7	4351	2 T00252	cadherin 5 precu
15	62	67.4	784	1 ITHUC5	N-cadherin 2 precu
16	62	67.4	877	1 ITHUCN	N-cadherin 2 precu
17	62	67.4	906	1 ITHUCN	N-cadherin 2 precu
18	62	67.4	906	1 ITHUCN	N-cadherin 2 precu
19	62	67.4	912	1 ITHUCN	N-cadherin 2 precu
20	61	66.3	913	1 A47543	R-cadherin precu
21	61	66.3	913	1 ITHUCR	R-cadherin precu
22	61	66.3	913	1 ITHUCR	R-cadherin precu
23	58	63.0	2610	2 T20968	hypothetical prote
24	57	62.0	4307	2 T20721	hypothetical prote
25	57	62.0	773	2 B38892	cadherin 13 precu
26	57	62.0	770	2 B48910	desmocollin 1b pre
27	57	62.0	840	2 A48910	desmocollin 1a pre
28	57	62.0	894	2 I37281	Descl precursor -
29	57	62.0	894	2 I37282	Descl precursor -
30	57	62.0	905	1 ITHUC1	N-cadherin 1 precu

30	57	62.0	906	1 ITHUC2	N-cadherin 2 precu
31	57	62.0	1715	2 JF0128	Bombay mori recept
32	57	62.0	3097	2 T00021	DN-cadherin - fru
33	57	62.0	3147	1 ITHUCW	cadherin-related t
34	56	60.9	373	2 T34563	hypothetical prote
35	56	60.9	882	1 ITHUCR	cadherin 1 precu
36	56	60.9	1069	2 T00043	BH-protocadherin-a
37	56	60.9	1072	2 T00041	BH-protocadherin-p
38	56	60.9	1200	2 T00042	T-cadherin precu
39	55	59.8	712	1 ITHUCR	T-cadherin precu
40	55	59.8	717	2 I51206	T-cadherin 2 - chi
41	55	59.8	886	2 I45858	desmocollin - bovi
42	55	59.8	3034	2 T14119	seven-pass transme
43	54	58.7	826	2 B55363	desmocollin, type
44	54	58.7	896	2 A55363	desmocollin, type
45	54	58.7	916	2 C38992	cadherin 4 precu

ALIGNMENTS

RESULT 1
G02678
cadherin-14 - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02678
R/Shindaba, T.; Shimoyama, Y.; Gotoh, N.; Hirohashi, S.
Submitted to the EMBL Data Library, May 1996
A/Reference number: H01584
A/Accession: G02678
A/Molecule type: mRNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-790 <SHI>
A/Cross-references: UNIPROT:Q13614; EMBL:U59325; NID:G1389652; PIDN:AA02933.1; PID:913
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSVDVNDNP 18
DB 249 SGSTVTVTLSVDVNDNP 266

RESULT 2

D38992
cadherin 8 - human
C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: D38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-793 <SUZ>
A/Cross-references: GB:U34060; NID:9506411; PIDN:AAA5628.1; PID:9506412
C/Genetics:
A/Gene: GDB:CDH8
A/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 793;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 250 SGTITVTLTVLTDVNDNPP 267

RESULT 3

150180
C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: 150180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: 150178; PMID:95309115; PMID:7540531
A/Accession: 150180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NA>
A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 89.1%; Score 82; DB 2; Length 785;
Best Local Similarity 83.3%; Pred. No. 7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 243 SGTIVTVTLTVNDNPP 260

RESULT 4

151638
F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: 151638; PMID:96039533; PMID:7496627
A/Accession: 151638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <ESP>
A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA59679.1; PID:98546
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 88.0%; Score 81; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 0.0001;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 248 AGTIVTVTLSDVNDNPP 265

RESULT 5

152701
K-cadherin - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 152701
R:Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara,
Cancer Res. 54, 3034-3041, 1994
A>Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A/Reference number: 152701; PMID:9423827; PMID:8187093
A/Accession: 152701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RES>

A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435460
A/Genetics: KCAD
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 789;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 249 SGTIVTVTLTVNDNPP 266

RESULT 6

150178
cadherin-6B - chicken
C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: 150178
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe
A/Reference number: 150178; PMID:95309115; PMID:7540531
A/Accession: 150178
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <NA>
A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 249 SGTIVTVTLTVNDNPP 266

RESULT 7

137016
cadherin-6 - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: 137016
R:Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A>Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the f
A/Reference number: 137016; PMID:95262134; PMID:7743525
A/Accession: 137016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
C/Genetics: GDB:CDH6

A/Cross-references: GDB:5822908
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
||:|||||:|||||
Db 249 SGTIVTVTLTVNDNPP 266

RESULT 8

A38992
Caderherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:I34056; NID:9506403; PIDN:AAA35622.1; PID:9506404
C/Genetics:
A/Gene: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/127-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
Best Local Similarity 77.8%; Pred. No. 0.00021;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
||:||||:|||||
Db 249 SGTTKVTITLTDVNDNP 266

RESULT 9
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hoffmann, I.; Belling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; MUID:95269886; PMID:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:96660
C/Genetics:
A/Gene: cad-11
C/Superfamily: cadherin; cadherin repeat homology
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
Best Local Similarity 77.8%; Pred. No. 0.00021;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
||:||||:|||||
Db 249 SGTTKVTITLTDVNDNP 266

RESULT 10
149556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R/Kimura, Y.; Matsumami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A/Title: Cadherin-11 expressed in mesenchymal morphogenesis in the head

A/Reference number: 149556; MUID:95269887; PMID:7750650
A/Accession: 149556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; GB:D31963; NID:9744190; PIDN:BA06730.1; PID:974419
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
Best Local Similarity 77.8%; Pred. No. 0.00021;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
||:||||:|||||
Db 249 SGTTKVTITLTDVNDNP 266

RESULT 11
A53584
OB-cadherin precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A53584
R/Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amann, E.
J. Biol. Chem. 269, 12092-12098, 1994
A/Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A/Reference number: A53584; MUID:94216322; PMID:163513
A/Accession: A53584
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-796 <OKA>
A/Cross-references: UNIPROT:P55288; GB:D21253; NID:9994774; PIDN:BA04797.1; PID:9994774
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: transmembrane protein
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
Best Local Similarity 77.8%; Pred. No. 0.00021;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
||:||||:|||||
Db 249 SGTTKVTITLTDVNDNP 266

RESULT 12
159372
cadherin 12 - human
N/Alternate names: Br-cadherin
C/Species: Homo sapiens (man)
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C/Accession: 159372
R/Selley, S.; Bruno, S.; Schaff, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.I.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A/Title: Expressed cadherin pseudogenes are localized to the critical region of the spl
A/Reference number: 159372; MUID:95249541; PMID:7731968
A/Accession: 159372
A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
A/Molecule type: mRNA
A/Residues: 1-794 <RES>
A/Cross-references: UNIPROT:P55289; GB:I33477; NID:9793942; PIDN:AAB48539.1; PID:9793942
C/Genetics:
A/Gene: GDB:CDH12
A/Cross-references: GDB:596324
A/Map position: 5p13-5p14
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F/57-160/Domain: cadherin repeat homology <CR1>
F/163-269/Domain: cadherin repeat homology <CR2>
F/272-384/Domain: cadherin repeat homology <CR3>

F:387-489/Domain: cadherin repeat homology <CR4>
 F:481-501/Domain: cadherin repeat homology <CR5>
 F:610-637/Domain: transmembrane #status predicted <TM>
 F:638-794/Domain: intracellular #status predicted <INT>

Query Match 77.2%; Score 71; DB 2; Length 794;
 Best Local Similarity 66.7%; Pred. No. 0.0039;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
 DB 250 AGTIVVITLTDVNDNP 267

RESULT 13
 T30213
 G-cadherin - sea urchin (Lytechinus variegatus)
 C/Species: Lytechinus variegatus (variegated urchin)
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30213
 R/Miller, J.R.; McClay, D.R.
 Dev. Biol. 192, 323-339, 1997
 A/Title: Characterization of the role of cadherin in regulating cell adhesion during sea
 A/Reference number: 220780; MUID:98104238; PMID:9441671
 A/Accession: T30213
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2809 <MIL>
 A/Cross-references: UNIPROT:O61230; EMBL:U34823; NID:92982186; PID:92982187; PIRN:AA063

Query Match 72.8%; Score 67; DB 2; Length 2809;
 Best Local Similarity 66.7%; Pred. No. 0.068;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
 DB 1694 SGATVAVTVDNDTP 1711

RESULT 14
 T00252
 MEGF1 protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T00252
 R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A/Reference number: 214126; MUID:98360089; PMID:9693030
 A/Accession: T00252
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-4351 <NAK>
 A/Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:93449285; PIDN:BAA32458.1; PID:93
 A/Experimental source: brain
 C/Genetics:

Query Match 70.7%; Score 65; DB 2; Length 4351;
 Best Local Similarity 61.1%; Pred. No. 0.23;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
 DB 2360 TGETLVVNVSDINDNP 2377

RESULT 15
 10HUCS

cadherin 5 precursor - human
 N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: S49893; S24305; A43418
 R/Breviario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Inzana, M.; Lamp
 submitted to the EMBL Data Library, June 1994
 A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
 A/Reference number: S49893

A/Accession: S49893
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-784 <BRE>
 A/Cross-references: UNIPROT:P3151; EMBL:X79981; NID:9599833; PIDN:CAA56306.1; PID:95998
 R/Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A/Reference number: S24305; MUID:91289540; PMID:2059658
 A/Accession: S24305
 A/Molecule type: mRNA
 A/Residues: 5-516; 'I', 518-784 <SUZ>
 A/Cross-references: EMBL:X59796; NID:9639976; PIDN:CAA42468.1; PID:929593
 R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Huenen, G.; Rucco,
 J. Cell Biol. 118, 1511-1522, 1992
 A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
 A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418
 A/Molecule type: protein
 A/Residues: 48-60; 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
 A/Experimental source: cultured endothelial cells
 A/Note: sequence extracted from NCBI backbone (NCBI:P:113040, NCBI:P:113045, NCBI:P:113047,
 C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
 C/Genetics:
 A/Gene: GDB:CDH5
 A/Cross-references: GDB:134230; OMIM:601120
 A/Map position: 16q22.1-16q22.1
 C/Suprafamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot
 F:1-25/Domain: signal sequence #status predicted <PRO>
 F:26-47/Domain: propeptide #status predicted <MAT>
 F:48-784/Domain: extracellular #status predicted <EXT>
 F:148-593/Domain: cadherin repeat homology <CR1>
 F:150-151/Domain: cadherin repeat homology <CR2>
 F:154-258/Domain: cadherin repeat homology <CR3>
 F:261-372/Domain: cadherin repeat homology <CR4>
 F:375-479/Domain: cadherin repeat homology <CR5>
 F:481-587/Domain: cadherin repeat homology <CR6>
 F:594-620/Domain: transmembrane #status predicted <TM>
 F:621-784/Domain: intracellular #status predicted <INT>
 F:736-753/Region: serine-rich
 F:61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 67.4%; Score 62; DB 1; Length 784;
 Best Local Similarity 66.7%; Pred. No. 0.1;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
 DB 239 SGATVAVTVDNDNP 256

Search completed: December 8, 2004, 10:27:08
 Job time: 2.45573 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 7.21488 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-12
Perfect score: 92
Sequence: 1 SGGTTVTLSDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	100.0	Q86T00	Q86T00 homo sapien
2	92	100.0	Q96LQ7	Q96LQ7 homo sapien
3	92	100.0	Q6PFX6	Q6PFX6 mus musculu
4	92	100.0	AAH57373	AAH57373 mus muscu
5	92	100.0	CAD0_HUMAN	CAD0_HUMAN
6	92	100.0	Q8BLB5	Q8BLB5 mus musculu
7	92	100.0	Q6PANA	Q6PANA mus musculu
8	92	100.0	AAH60200	AAH60200 mus muscu
9	92	100.0	Q8C375	Q8C375 mus musculu
10	92	100.0	Q8C449	Q8C449 mus musculu
11	92	100.0	AAH57581	AAH57581 mus muscu
12	92	100.0	Q8BRK4	Q8BRK4 mus musculu
13	92	100.0	CAD1_HUMAN	CAD1_HUMAN
14	92	100.0	CAD8_HUMAN	CAD8_HUMAN
15	92	100.0	CAD8_MOUSE	CAD8_MOUSE
16	92	100.0	CAD8_RAT	CAD8_RAT
17	92	100.0	Q8BLT4	Q8BLT4 mus musculu
18	92	100.0	Q8AMW2	Q8AMW2 mus musculu
19	92	100.0	Q81Y78	Q81Y78 homo sapien
20	92	100.0	CAD7_CHICK	CAD7_CHICK
21	92	100.0	CAD7_HUMAN	CAD7_HUMAN
22	92	100.0	Q8BM92	Q8BM92 mus musculu
23	92	100.0	Q91838	Q91838 xenopus lae
24	92	100.0	CADA_HUMAN	CADA_HUMAN
25	92	100.0	Q80WS7	Q80WS7 mus musculu
26	92	100.0	Q8V168	Q8V168 mus musculu
27	92	100.0	AAH62962	AAH62962 mus muscu
28	92	100.0	CAD6_RAT	CAD6_RAT
29	92	100.0	CADA_CHICK	CADA_CHICK
30	92	100.0	CAD6_CHICK	CAD6_CHICK
31	92	100.0	CAD6_HUMAN	CAD6_HUMAN

32	80	87.0	790	1	CAD6_MOUSE	P97326 mus musculu
33	80	87.0	798	2	Q8ZVY7	Q8ZVY7 gallus gall
34	80	87.0	798	2	Q8GCH3	Q8GCH3 gallus gall
35	80	87.0	801	1	CADK_HUMAN	Q9H26 homo sapien
36	80	87.0	801	2	Q9Z0M3	Q9Z0M3 mus musculu
37	80	87.0	813	1	CADM_MOUSE	Q9WTP5 mus musculu
38	80	87.0	813	1	CADM_RAT	Q6315 ratcus norv
39	80	87.0	828	1	CADM_HUMAN	Q9U19 homo sapien
40	79	85.9	792	1	CADH_CHICK	Q9319 gallus gall
41	79	85.9	794	2	Q93264	Q93264 xenopus lae
42	79	85.9	796	1	CADH_HUMAN	P55287 homo sapien
43	79	85.9	796	1	CADH_MOUSE	P55288 mus musculu
44	79	85.9	796	2	Q8C706	Q8C706 mus musculu
45	75	81.5	789	1	CAD9_HUMAN	Q9UB4 homo sapien

ALIGNMENTS

RESULT 1	Q86T00	PRELIMINARY;	PRT;	370 AA.
ID	Q86T00			
AC	Q86T00			
DT	01-JUN-2003 (TREMBlrel. 24, Created)			
DT	01-JUN-2003 (TREMBlrel. 24, Last sequence update)			
DE	Full-length cDNA clone CS0DX003Y017 of Hela cells of Homo sapiens (human) (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hela cells;			
RA	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
RA	Genoscope;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hela cells;			
RA	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
CC	EMBL; BX248303; CAD62530.1;			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0007156; F:homophilic cell adhesion; IEA.			
DR	InterPro; IPR002126; Cadherin.			
DR	Pfam; PF00028; Cadherin; 3.			
DR	PRINTS; PR00205; CADHERIN.			
DR	SMART; SMO0112; CA_2.			
DR	PROSITE; PS00232; CADHERIN_1; 1.			
DR	PROSITE; PS50268; CADHERIN_2; 4.			
KW	Calcium; Calcium-binding.			
FT	NON_TER 1			
FT	NON_TER 370			
SQ	SEQUENCE 370 AA; 39479 MW; 399604AF8A500E0 CRC64;			
Query Match	100.0%; Score 92; DB 2; Length 370;			
Best local Similarity	100.0%; Pred. No. 4.7e-06;			
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
CY	1 SGGTTVTLSDVNDNP 18			
DB	1 SGGTTVTLSDVNDNP 18			
RESULT 2	Q96LQ7	PRELIMINARY;	PRT;	493 AA.
ID	Q96LQ7			
AC	Q96LQ7			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			

```

DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
OS Hypothetical protein FLJ25193.
DE Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimmiya K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura T., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sogano S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL; AK057922; BAB71613.1; -
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:phospholipid cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00205; Cadherin; 4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS00268; CADHERIN_2; 4.
KW Calcium; Calcium-binding;
SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 92; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 6; se-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVLSDVNDNPP 18
DB 240 SGGTIVTVLSDVNDNPP 257

|||||
ID AHS57373 PRELIMINARY; PRT; 781 AA.
AC Q6PFX6
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cadherin-like 24.
GN Name=CDH24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

```

```

RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; BC057373; AHS57373.1; -
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR00233; Cadherin_C-term.
DR Pfam; PF00205; Cadherin; 5.
DR Pfam; PF01049; Cadherin; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS00268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1; le-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVLSDVNDNPP 18
DB 240 SGGTIVTVLSDVNDNPP 257

|||||
ID AHS57373 PRELIMINARY; PRT; 781 AA.
AC AHS57373
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cadherin-like 24.
GN CDH24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strauberg R.;
RL Submitted (Sep-2003) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

Query March 100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Dh 240 SGGSTTVTLSDVNDNPP 257
1 SGGSTTVTLSDVNDNPP 18

RESULT 5
ID CADO_HUMAN STANDARD; PRT; 819 AA.
AC Q86UP0; Q86UP1; Q9NT84;
CD 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CATENINS.
RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Kateliasz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
II cadherin";
RJ J. Biol. Chem. 278:27513-27519(2003).

RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Choi C., Crowley C., Currell B., Deuel B., Dowd P.,
Batton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld U.,
Seisagiri S., Simmons L., Singh U., Smith V., Stinson J., Vargas A.,
Vanalen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yasura D.,
Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment";
RZ Genome Res. 13:2265-2270(2003).

RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Testis;
RA Blum H., Banerach S., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (Jan-2000) to the EMBL/GenBank/DBJ database.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types. Cadherin-24 mediate strong
cell-cell adhesion.
-1- SUBUNIT: Associates with alpha-, beta- and delta-catennins.
-1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=Long form;
IsoId=Q86UP0-1; Sequence=1isplayed;
Name=2; Synonyms=Short form;
IsoId=Q86UP0-2; Sequence=VSP_008717;
Name=3;
IsoId=Q86UP0-3; Sequence=VSP_008718, VSP_008719;
CC

```

CC CC Note=No experimental confirmation available;
CC -I- SIMILARITY: Contains 5 cadherin domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC -----
CC EMBL; AY260590; AAP20590.1; --
CC EMBL; AY260591; AAP20591.1; --
CC EMBL; AY358199; AAQ88566.1; --
CC EMBL; AL137477; CAB70758.1; --
CC PIR; T46418; T46418.
CC HSSP; P09803; I17W.
CC Genew; HGNC:14265; CDH24.
CC InterPro; IPRO02126; Cadherin_C_term.
CC InterPro; IPRO00233; Cadherin_5.
CC Pfam; PF00280; Cadherin; 5.
CC Pfam; PF01049; Cadherin_C; 1.
CC PRINTS; PR00235; CADHERIN.
CC PROSITE; PS00233; CADHERIN_1; 2.
CC PROSITE; PS02068; CADHERIN_2; 5.
CC KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
    Multigene family; Repeat; Signal; Transmembrane.
    FT SIGNAL 1 19 Potential.
    FT PROPEP 21 44 Potential.
    FT CHAIN 45 819 Cadherin-24.
    FT DOMAIN 45 641 Extracellular (Potential).
    FT TRANSHEM 642 662 Potential.
    FT DOMAIN 663 819 Cytoplasmic (Potential).
    FT DOMAIN 46 150 Cadherin 1.
    FT DOMAIN 151 259 Cadherin 2.
    FT DOMAIN 260 374 Cadherin 3.
    FT DOMAIN 375 517 Cadherin 4.
    FT DOMAIN 517 630 Cadherin 5.
    FT CARBOHYD 446 446 N-linked (GLCNAC...) (Potential).
    FT CARBOHYD 548 548 N-linked (GLCNAC...) (Potential).
    FT CARBOHYD 563 563 N-linked (GLCNAC...) (Potential).
    FT VASPLIC 455 492 Missing (in isoform 2).
    FT VASPLIC 455 492 /FtId=VSP_008717.
    FT VASPLIC 1 427 Missing (in isoform 3).
    FT VASPLIC 428 492 /FtId=VSP_008718.
    FT VASPLIC 428 492 ECTHTAPLRREARRAMNLTVALTELGMSCGPERGWYBL
        VAEMSAAPARPQRSPUGAVGIPO -> MNIVTCWYSIH
        ATLPSFTLHAIFMCFCLMLYASCGIHHAAHPMLRVNVCYC
        VMRVCFGVLPS (in isoform 3).
        /FtId=VSP_008719.
SQ SEQUENCE 819 AA; 87751 MW; 9083034FI8BA7EA4 CRC64;
QY 1 SGSTVTVTLSVDNDNP 18
Db 240 SGSTVTVTLSVDNDNP 257
Query Match 100.0%; Score 92; DB 1; Length 819;
Best Local Similarity 100.0%; Pred. NO. 1.le-05; Indels 0; Gaps 0
Matches 18; Conservative 0; Mismatches 0;

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Suno H., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 genome sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Boro H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nihi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1. SIMILARITY: Contains 3 cadherin domains.
 DR EMBL; AK045672; BAC32451.1; -
 DR HSSP; P15116; INCU
 DR MGI; 2444914; B230202171K.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 3.
 DR PRINTS; PR00205; CADHERIN.

DR SMART; SM00112; CA_2
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 3.
 KW Calcium; Calcium-binding; Hypothetical protein.
 FT NON TER 337 337
 SQ SEQUENCE 337 AA; 37137 MW; C81B98A3038FA10C CRC64;
 Query Match 90.2%; Score 83; DB 2; Length 337;
 Best Local Similarity 83.3%; Pred. No. 0.00011;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SGGSTTVTLSDVNDNPP 18
 Db 249 SGGSTTVNITLTDVNDNPP 266
 RESULT 7
 ID O6PAN4 PRELIMINARY; PRT; 508 AA.
 AC O6PAN4;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whittinger M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1. SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA_4
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 4.
 KW Calcium; Calcium-binding.
 SQ SEQUENCE 508 AA; 56388 MW; 9053F74BCF52255 CRC64;
 Query Match 90.2%; Score 83; DB 2; Length 508;
 Best Local Similarity 83.3%; Pred. No. 0.00011;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGSTTVTLSDVNDNPP 18

```

DB      257  SGTTLVT/LTVNDVNDNP 274
||||:||||:||||:
RESULT 8
AAH60200 PRELIMINARY; PRT; 508 AA.
ID      AAH60200;
AC      AAH60200;
DT      02-MAR-2004 (TREMBlrel. 27, Created)
DT      02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT      02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE      Cdh8 protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RC      MEDLINE=2238257; PubMed=12477932;
RA      Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buettner K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stalcup M., Soares W.B., Bontaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA      Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA      Kravitz M.T., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Merra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RT      [Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).]
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RC      Strussberg R.;
RA      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC060200; AAH60200.1; -
SQ      SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;

Query Match      90.2%; Score 83; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 0.00018;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY      1  SGTTLVT/LTVNDVNDNP 18
DB      257  SGTTLVT/LTVNDVNDNP 274
||||:||||:||||:
RESULT 9
08C375 PRELIMINARY; PRT; 716 AA.
ID      08C375;
AC      08C375;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DE      library, clone:ID30046N17 product:cadherin 8, full insert
DE      sequence.
GN      Name=Cdh8;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=99279253; PubMed=10349636;
RA      Carninci P., Hayashizaki Y.;
RA      "High-efficiency full-length cDNA cloning."
RA      Meth. Enzymol. 303:13-44 (1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=21085660; PubMed=11217851;
RA      RIKEN FANTOM Consortium;
RA      "Functional annotation of a full-length mouse cDNA collection."
RA      Nature 409:685-690 (2001).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RA      The FANTOM Consortium;
RA      "Analysis of the mouse transcriptome based on functional annotation of
RA      60,770 full-length cDNAs."
RA      Nature 420:563-573 (2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=2049374; PubMed=11042159;
RA      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA      Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RA      "Normalization and subcloning of cap-trapper-selected cDNAs to
RA      prepare full-length cDNA libraries for rapid discovery of new genes."
RA      Genome Res. 10:1617-1630 (2000).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=20530913; PubMed=11076861;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA      Smit N., Ishii Y., Nakamura S., Hazama M., Nishime T., Harada A.,
RA      Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA      Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA      Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA      Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT      "RIKEN integrated sequence analysis (RISA) system-384-format
RT      sequencing pipeline with 384 multiloopillary sequencer."
RT      Genome Res. 10:1757-1771 (2000).
RN      [6]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RA      Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA      Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA      Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA      Hori F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA      Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA      Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura Y.,
RA      Nishi K., Nomura K., Numataki R., Ohno M., Ohsato N., Okazaki Y.,
RA      Saito R., Saiton H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA      Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA      Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA      Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA      Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN      [7]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RA      "SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
RA      -1 SIMILARITY: Contains 5 cadherin domains.
RA      EMBL; AK086711; BAC39724.1; -
RA      HESP; P15116; INCF.
RA      MGD; MGI:107434; Cdh8.
RA      GO; GO:0016020; C:membrane; IEA.
RA      GO; GO:0005509; F:calcium ion binding; IEA.
RA      GO; GO:0007156; P:homophilic cell adhesion; IEA.
RA      InterPro; IPR002126; Cadherin.
RA      InterPro; IPR000233; Cadherin_C_term.
RA      Pfam; PF00028; Cadherin; 5.
RA      Pfam; PF01049; Cadherin_C; 1.

```

DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79149 MW; 5BBD558F63862A4 CRC64.

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 SGSTVTVTLSDVNDNPP 18
 |||:|||||:
 Db 257 SGTTLTVTLVDVNDNP 274

RESULT 10
 O8C449 PRELIMINARY; PRT; 716 AA.
 AC O8C449;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone:CE30002D14 product:cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID:10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komano H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komano H., Akiyama J., Nishi K., Kitajima T., Tashtiro H., Itoh M.,
 RA Sunti N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hasegawa T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Komano H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grose L.H., Derge J.G.,
 RA Krausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo K.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; AK083092; BAC38758.1; -;
 DR EMBL; BC057581; AA57581.1; -;
 DR HSSP; P5116; INCI.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 SGSTVTVTLSDVNDNPP 18
 |||:|||||:
 OY |||:|||||:

DB 257 SGTTLVTLVDVNDNP 274

RESULT 11

AAH57581 PRELIMINARY; PRT; 716 AA.

AC 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Strassle M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughele N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Wozniak K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez M.L., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Merritt W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057581; AAH57581.1;
 SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTLVDVNDNP 18
 DB 257 SGTTLVTLVDVNDNP 274

RESULT 12
 Q8BRK4 PRELIMINARY; PRT; 754 AA.

AC 08BRK4;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 library, clone:AB30083P13 product:cadherin 8, full insert
 sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;

RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA The PANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koyama M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeuchi Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK044046; BAC11751.1; -;
 DR HSSP; P15116; INCU.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0071156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002333; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01043; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.

DR PROSITE; PS50268; CADHERIN 2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 754 AA, 83624 MW, 149C3C70D3F21568 CRC64.

Query Match 90.2%; Score 83; DB 2; Length 754;
 Best Local Similarity 83.3%; Pred. No. 0.00028;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVLSDVNDNP 18
 |||:|||||:|||||
 Db 257 SGTITVITLTDVNDNP 274

RESULT 13
 CADI_HUMAN STANDARD; PRT; 790 AA.
 AC Q13634;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Cadherin-18 precursor (Cadherin-14).
 GN Name=CDH18; Synonyms=CDH14;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184182; PubMed=9030594;
 RA Shibata T., Shimoyama Y., Gotoh M., Hirohashi S.;
 RT "Identification of human cadherin-14, a novel neurally specific type
 II cadherin, by protein interaction cloning.";
 RL J. Biol. Chem. 272:5236-5240(1997).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; U59325; AAB02933.1; -;
 DR PIR; G02678; G02678.
 DR HSSD; P09803; 117X.
 DR Genew; HGNC:1757; CDH18.
 DR MIM; 603019; -;
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002033; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA_5
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 790 Cadherin-18.
 FT DOMAIN 54 608 Extracellular (Potential).
 FT TRANSMEM 609 636 Potential.
 FT DOMAIN 637 790 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.

FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 790 AA; 88072 MW, 5C7BDEB229B6EDCA CRC64;

Query Match 90.2%; Score 83; DB 1; Length 790;
 Best Local Similarity 83.3%; Pred. No. 0.0003;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVLSDVNDNP 18
 |||:|||||:|||||
 Db 249 SGTITVITLTDVNDNP 266

RESULT 14
 CADI_HUMAN STANDARD; PRT; 799 AA.
 AC P5286; Q9UBH2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitejima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.";
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Taniguchi H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Retal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Taniguchi H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 7.44864 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-12

Perfect score: 92

Sequence: 1 SGSTTVTVTLSDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 segs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	92	100.0	18	7	ADD29453 Human cad
2	92	100.0	18	7	ADD29452 Human cad
3	92	100.0	493	5	AD116946 Human NOV
4	92	100.0	607	5	ABBS3295 Human NOV
5	92	100.0	620	7	ADD29448 Human cad
6	92	100.0	636	7	ADD29445 Human cad
7	92	100.0	781	5	ABBS3296 Human pol
8	92	100.0	781	5	AMM48735 Human cad
9	92	100.0	781	5	ABG34078 Human pro
10	92	100.0	781	5	AD116604 Human NOV
11	92	100.0	781	5	AD116606 Human NOV
12	92	100.0	781	6	ABR40114 Human cel
13	92	100.0	781	6	ADA01366 Human PRO
14	92	100.0	781	6	ADA43795 Human sec
15	92	100.0	781	6	ADA43563 Human sec
16	92	100.0	781	6	ADA01238 Human PRO
17	92	100.0	781	7	ADA01122 Human sec
18	92	100.0	781	7	ADA43679 Human sec
19	92	100.0	781	7	ADA06941 Human PRO
20	92	100.0	781	7	ADA08429 Human PRO
21	92	100.0	781	7	ADBS9722 Human PRO
22	92	100.0	781	7	ADBS87005 Human PRO
23	92	100.0	781	7	ADBS65160 Human sec
24	92	100.0	781	7	ADBS98858 Human PRO
25	92	100.0	781	7	ADBS99493 Human hum

26	92	100.0	781	7	ADB66044 Human sec
27	92	100.0	781	7	ADC23442 Human tra
28	92	100.0	781	7	ADC26135 Human PRO
29	92	100.0	781	7	ADG04962 Human PRO
30	92	100.0	781	7	ADG11268 Human PRO
31	92	100.0	781	7	ADDB8199 Human PRO
32	92	100.0	781	7	ADD95494 Human sec
33	92	100.0	781	7	ADG06424 Human PRO
34	92	100.0	781	7	ADG38199 Human PRO
35	92	100.0	781	7	ADD88315 Human PRO
36	92	100.0	781	7	ADD90896 Human sec
37	92	100.0	781	7	ADG99451 Human PRO
38	92	100.0	781	7	ADG06544 Human PRO
39	92	100.0	781	7	ADG05495 Human PRO
40	92	100.0	781	7	ADG82496 Human PRO
41	92	100.0	781	8	ADG51749 Human sec
42	92	100.0	781	8	ADG51865 Human sec
43	92	100.0	781	8	ADG37723 Human sec
44	92	100.0	781	8	ADG37607 Human sec
45	92	100.0	781	8	ADD95378 Human sec

ALIGNMENTS

RESULT 1
ADD29453
ID ADD29453 standard; peptide; 18 AA.
XX
AC ADD29453:
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID12.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytoskeletal; osteopetrosis; cancer;
KW osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US200314491-A1.
XX
FD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GDB/) GODBOLE S D.
PA (KIOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALB/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
XX
XX WPI; 2003-829799/77.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteopetrosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 12; 63bp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, CC hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA;

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSPVNDNPP 18
Db 1 SGGTIVTVTLSPVNDNPP 18

RESULT 2

ADD29452 ID ADD29452 standard; peptide; 18 AA.

AC ADD29452;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein peptide fragment Seq ID11.

KM cadherin-like protein; transmembrane protein; cadherin domain;

KM homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;

KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;

KM metastatic tumour; human.

XX Homo sapiens.

OS US2003144491-A1.

PN 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00469314.

PR 27-APR-2000; 2000US-00560875.

PA (GDB/) GODBOLE S D.

PA (KDOC/) KOC C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI, 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 11; 63bp; English.

CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, CC hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA;

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSPVNDNPP 18
Db 1 SGGTIVTVTLSPVNDNPP 18

RESULT 3

AD116946 ID AD116946 standard; protein; 493 AA.

AC AD116946;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SeqID 482.

KM human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

KM inflammation; autoimmune disorder; allergy; blood disorder;

KM acquired immunodeficiency syndrome; AIDS; obesity; asthma;

KM immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;

KM Alzheimer's disease; infection; str.

XX Homo sapiens.

OS WO200268649-A2.

PN 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 31-JAN-2001; 2001US-0265517P.

PR 02-FEB-2001; 2001US-0266406P.

PR 05-FEB-2001; 2001US-0266767P.

PR 07-FEB-2001; 2001US-0266975P.

PR 08-FEB-2001; 2001US-0267057P.

PR 09-FEB-2001; 2001US-0267459P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 02-MAR-2001; 2001US-0271855P.

PR 14-MAR-2001; 2001US-0272788P.

PR 02-MAR-2001; 2001US-0273046P.

PR 14-MAR-2001; 2001US-0275925P.

PR 14-MAR-2001; 2001US-0275947P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276397P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278775P.

PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001, 2001US-0279884F, PR
PR 30-MAR-2001, 2001US-0280147F, PR
PR 11-APR-2001, 2001US-0282992F, PR
PR 11-APR-2001, 2001US-0283083F, PR
PR 20-APR-2001, 2001US-0285133F, PR
PR 23-APR-2001, 2001US-0285749F, PR
PR 03-MAY-2001, 2001US-0288327F, PR
PR 03-MAY-2001, 2001US-0288504F, PR
PR 29-MAY-2001, 2001US-0294047F, PR
PR 30-MAY-2001, 2001US-0294473F, PR
PR 08-JUN-2001, 2001US-0296564F, PR
PR 18-JUN-2001, 2001US-0296859F, PR
PR 19-JUN-2001, 2001US-0299324F, PR
PR 13-AUG-2001, 2001US-0312020F, PR
PR 16-AUG-2001, 2001US-0312889F, PR
PR 16-AUG-2001, 2001US-0312908F, PR
PR 21-AUG-2001, 2001US-0313390F, PR
PR 28-AUG-2001, 2001US-0315470F, PR
PR 31-AUG-2001, 2001US-0316447F, PR
PR 07-SEP-2001, 2001US-0318115F, PR
PR 07-SEP-2001, 2001US-0318118F, PR
PR 12-SEP-2001, 2001US-0318740F, PR
PR 19-SEP-2001, 2001US-0323379F, PR
PR 18-OCT-2001, 2001US-03303245F, PR
PR 18-OCT-2001, 2001US-0330308F, PR
PR 14-NOV-2001, 2001US-0332701F, PR

PA (CURA-) CURAGEN CORP.
 XX
 PA Tchernev VT, Selyek KA, Zernhusen BD, Patruzajan M, Shinkets RA;
 PI Li L, Gargolli EA, Padigan M, Anderson SM, Rastelli L, Miller CE;
 PI Li L, Gaighan VI, Taupier RJ, Gusev VY, Colman SD, Wolencik AR, Pena CEa,
 PI Futak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE,
 XX
 DR WPI; 2002-706998/76.
 XX
 XX New NOVA polypeptides and nucleic acids, useful for preventing or
 PT treating NOVA-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Disclosure; SEQ ID NO 482; 1498bp; English.

CC This invention relates to a novel nucleic acid and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy,
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antirheumatoid, anorectic,
CC antiaesthetic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.

SQ Sequence 493 AA;

QY	1	SGSTVTVTLSDVNDNPP	18
Db	240	SGSTVTVTLSDVNDNPP	257

Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
ABB53295
ID ABB53295 standard; protein; 607 AA

AC ABB532957

DT 12-FEB-2002 (first entry)

Human polypeptide #35.

Human: neurotropic; neuropro-ective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquiliser; antihypertensive; diuretic; antidiabetic;
 KM antiinflammatory; antidiabetic; hepatotropic; virocid; antidiabetic;
 KM nephrotoxic; anorectic; cytosarctic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease
 OS Homo sapiens.
 XX

PN WO200181363-A1

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 25-MAY-2000; 2000US-0207087P.
00 MAY 2000 2000ITB-0207E46P

XX
 (SMY) SMYTHINE BEECHAM CORP
 11

PA (SMIK) SMITHKLINE BEECHAM PLC.

Pt	Agarwal P,	Murdock PR,	Rizvi SK,	Smiten RF,	Alding Z,	Kadnikov AS,
Pt	Taj Y	Xie O:				

XX
XX
WDT: 2003-041302/05

DR N-PSDB; ABA90360.
YY

Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated with the polypeptide, e.g., Alzheimer's

PT disease, dyslipidemia, obesity, diabetes

PS Claim 1; Page 106-108; 116pp; English.
XX

CC THE INVENTION relates to an isolated polypeptide compound
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,

CC	844,	782,	202,	334,	711,	100,	200,	222,	122,	200,
CC	784,	252,	593,	472,	607,	781,	640,	686 or 154 amino acid sequence as		

polypeptides and antibodies against the polypeptides are useful for

Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic

congestive heart failure, Hodgkin's disease and myocardial infarction;

disease, cystic fibrosis and adult respiratory distress syndrome; liver

CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;

glomerulonephritis; skeletal muscle diseases including Eulenburg's

CC myotonia congenita and intestinal obstruction; lymph diseases including

CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility, and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 607 AA;

Query Match 100.0%; Score 92; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 240 SGSTVTVTLSDVNDNPP 257

RESULT 5

ADD29448
ID ADD29448 standard; protein; 620 AA.

AC ADD29448;
XX
XX
DT 15-JAN-2004 (first entry)

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

OS Homo sapiens.

XX US2003144491-A1.

PN 31-JUL-2003.

PD 16-FEB-2001; 2001US-00788051.

PF 03-FEB-2000; 2000US-00436914.

PR 27-APR-2000; 2000US-00560875.

XX (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

XX

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

XX

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX

PS Claim 11; SEQ ID NO 7; 63pp; English.

XX

CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutic useful for the treatment of diseases

CC such as cancers, osteoporosis, Paget's disease, osteomalacia,

CC hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic

CC tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the
CC invention.

XX
SQ Sequence 620 AA;

Query Match 100.0%; Score 92; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 224 SGSTVTVTLSDVNDNPP 241

RESULT 6

ADD29445
ID ADD29445 standard; protein; 636 AA.

AC ADD29445;
XX
XX
DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..16

FT Protein /label=Signal_peptide

FT 17..636

FT /label=Mature_human_cadherin-like_protein

PN US2003144491-A1.

PD 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00436914.

PR 27-APR-2000; 2000US-00560875.

XX (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

XX

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

XX

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX

PS Claim 11; SEQ ID NO 4; 63pp; English.

XX

CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutics useful for the treatment of diseases
CC such as cancer, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

XX Sequence 636 AA;

QY Query Match 100.0%; Score 92; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 SGGTTVTTLSDVNDNPP 18
240 SGGTTVTTLSDVNDNPP 257

RESULT 7
ABBS3296
ID ABBS3296 standard; protein; 781 AA.

XX ABBS3296;

DT 12-FEB-2002 (first entry)

XX Human polypeptide #36.

XX Human; nocrotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic;
XX antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
XX nephrotropic; anorectic; cytosolic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-0203336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX WPI: 2002-041392/05.

XX N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
XX disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX Claim 1, Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 784, 782, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including
XX Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
XX dystrophy, anorexia and depression; cardiovascular diseases including

CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Furlberg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphoglycemia; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

QY Query Match 100.0%; Score 92; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 SGGTTVTTLSDVNDNPP 18
240 SGGTTVTTLSDVNDNPP 257

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

XX AAM48736;

DT 28-MAR-2002 (first entry)

XX Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarrhythmic; antineuritic;
XX dermatological; immunosuppressive; antiinflammatory; antipruritic;
XX antidiabetic; antiallergic; antileptotic; haemostatic; antipruritic;
XX antihypertensive; antidiabetic; vasotropic; cardiant; antiarrhythmic;
XX anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016013.

XX 19-MAY-2000; 2000US-0205674P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI: 2002-083082/11.

XX N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for
XX diagnosing and treating disorders e.g. obstructive jaundice, multiple
XX sclerosis, encephalomyelitis and atherosclerosis and to identify
XX modulators of therapeutic use.

XX Claim 9, Page 105; 119pp; English.

XX The invention relates to human cadherin family polypeptide designated

CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarthritis, antirheumatic, dermatological,
 CC immunosuppressive, antiinflammatory, antipruritic, antiasmatic,
 CC antiallergic, antipruritic, haemostatic, antipruritic, antihypertensive,
 CC antihypertensive, antihypertensive, antihypertensive, antihypertensive,
 CC immunomodulatory, vasorelaxant, vasorelaxant, vasorelaxant, vasorelaxant,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy, cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy, liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

XX Sequence 781 AA;

Query Match

Best Local Similarity 100.0%; Score 92; DB 5; Length 781;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSPVNDNP 18
 DB 240 SGGSTVTVTLSPVNDNP 257

RESULT 9
 ABG34078 standard: protein; 781 AA.

XX 15-JUL-2002 (first entry)

XX Human Pro peptide #49.

XX Human, PRO, secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.

XX Homo sapiens.

XX WO200224888-A2.

XX 28-MAR-2002.

XX 29-AUG-2001; 2001WO-US027099.

XX 01-SEP-2000; 2000US-0228989P.

XX 05-SEP-2000; 2000US-0230621P.

XX 22-SEP-2000; 2000US-0235147P.

XX 10-NOV-2000; 2000WO-US030873.

XX 12-JAN-2001; 2001US-0261878P.

XX 16-JAN-2001; 2001US-0261910P.

XX 16-JAN-2001; 2001US-0261939P.

XX 25-JAN-2001; 2001US-0264395P.

XX 02-FEB-2001; 2001US-0266423P.

XX 09-FEB-2001; 2001US-0267623P.

XX 28-FEB-2001; 2001WO-US006520.

XX 09-MAR-2001; 2001US-0274399P.

XX 03-APR-2001; 2001US-0280982P.

XX 04-APR-2001; 2001US-0282129P.

XX 09-MAY-2001; 2001US-0290589P.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX (GENT) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Salth V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI; 2002-362426/39.
 DR N-PDB; AER70009.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX Claim 11; Fig 98, 218pp; English.
 CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention

XX Sequence 781 AA;

Query Match 100.0%; Score 92; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSPVNDNP 18
 DB 240 SGGSTVTVTLSPVNDNP 257

RESULT 10

AD116604
 ID AD116604 standard: protein; 781 AA.

XX 15-APR-2004 (first entry)

XX Human NOVX protein to treat human pathological conditions SeqID140.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytostatic; cardiant; antiinflammatory; immunosuppressive; anti-allergic;
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
 KW antistimatic; nephrotropic; antiarthritis; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.
OS
XX
PN WO200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002WO-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267453P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276788P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278778P.
PR 26-MAR-2001; 2001US-0278788P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282922P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0286827P.
PR 03-MAY-2001; 2001US-0286804P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312869P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX
PA (CURA-) CURAGEN CORP.
XX
XX Tchernev VT, Szytek KA, Zernhusen BD, Patturajan M, Shinkens RA;
PI Li L, Ganggoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Futak K, Grose WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX
DR WPI; 2002-706998/76.
DR N-PSDB; ADI16603.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Claim 1; SEQ ID NO 140; 1498pp; English.
XX
XX
CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytosolic, cardiac, anti-inflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiaesthetic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, neurotropic, antibacterial, vitreous, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 92; DB 5; Length 781;
Best local similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTTVTYISDVNDNPP 18
DB 240 SGGTTVTYISDVNDNPP 257
RESULT 11
ADI16606
ID ADI16606 standard; protein; 781 AA.
XX
XX
AC ADI16606;
XX
XX 15-APR-2004 (first entry)
DT
DE Human NOVX protein to treat human pathological conditions SeqID142.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cytostatic; cardiac; anti-inflammatory; immunosuppressive; antiallergic;
XX haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antiaesthetic; nephrotropic; antiarthritic; hepatotropic;
XX neuroprotective; neurotropic; antibacterial; vitreous; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
XX chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX
XX WO200268649-A2.
XX
XX 06-SEP-2002.

PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCYTE GENOMICS INC.
 PI Burford N, Warren BA, Dugan BM, Mason PW, Richardson TW, Yue H;
 PI Forsythe JF, Elliott VS, Griffin JA, Gorvay AE, Azimzai Y;
 PI Kallack DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 XX
 DR WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 PS
 PS Claim 1; Page 192-194; 234pp; English.
 CC
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 XX Sequence 781 AA;

QY Query Match 100.0%; Score 92; DB 6; Length 781;
 DB Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SGGTTVTTLSDVNDNP 18
 240 SGGTTVTTLSDVNDNP 257

RESULT 13
 ADA01366
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteoporosis; antineumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 XX 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.

XX (GENTECH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 PS
 PS Claim 11; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.

QY Query Match 100.0%; Score 92; DB 6; Length 781;
 DB Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SGGTTVTTLSDVNDNP 18
 240 SGGTTVTTLSDVNDNP 257

RESULT 14
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytosstatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003064474-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX MPI; 2003-605867/57.
DR N-PSDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumor in a mammal, including tumors of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGSTVTVTLSVDVNDNP 18
DB 240 SGSTVTVTLSVDVNDNP 257
RESULT 15
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX ADA43563;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX Human secreted/transmembrane polypeptide PRO34009.
XX DE
XX

KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumor; lung tumor; colon tumor;
KW breast tumor; prostate tumor; rectal tumor; kidney tumor;
KW liver tumor; cytostatic; vaccine.
XX Homo sapiens.
XX US2003073196-A1.
XX
XX 17-APR-2003.
XX
XX 18-SEP-2002; 2002US-00246210.
XX
XX 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX MPI; 2003-743814/70.
DR N-PSDB; ADA43562.
XX
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS Claim 11; Fig 98; 307pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumor in a mammal, including tumors of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGSTVTVTLSVDVNDNP 18

Wed Dec 8 11:46:21 2004

us-09-788-051-12.rag

Page 11

Db 240 SGGTTVTVTLSDVNDNPP 257

Search completed: December 8, 2004, 10:13:06
Job time : 7.44864 secs

This Page Blank (uspic),

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 18.3932 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-12
Perfect score: 92
Sequence: 1 SGSTVTVTLSDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgnt2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgnt2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgnt2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgnt2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgnt2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgnt2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgnt2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgnt2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgnt2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgnt2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgnt2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgnt2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgnt2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgnt2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgnt2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgnt2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgnt2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgnt2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgnt2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgnt2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	92	100.0	18	US-09-788-051-11	Sequence 11, Appl
2	92	100.0	18	US-09-788-051-12	Sequence 12, Appl
3	92	100.0	493	US-10-072-013-482	Sequence 482, App
4	92	100.0	607	US-10-258-951-74	Sequence 74, Appl
5	92	100.0	620	US-09-788-051-7	Sequence 7, Appl
6	92	100.0	636	US-09-788-051-4	Sequence 4, Appl
7	92	100.0	781	US-09-860-868-2	Sequence 2, Appl
8	92	100.0	781	US-10-245-752-98	Sequence 98, Appl
9	92	100.0	781	US-10-245-859-98	Sequence 98, Appl
10	92	100.0	781	US-10-245-103-98	Sequence 98, Appl
11	92	100.0	781	US-10-245-107-98	Sequence 98, Appl
12	92	100.0	781	US-10-245-143-98	Sequence 98, Appl
13	92	100.0	781	US-10-245-771-98	Sequence 98, Appl

14	92	100.0	781	US-10-245-851-98	Sequence 98, Appl
15	92	100.0	781	US-10-245-883-98	Sequence 98, Appl
16	92	100.0	781	US-10-237-535-98	Sequence 98, Appl
17	92	100.0	781	US-10-238-183-98	Sequence 98, Appl
18	92	100.0	781	US-10-238-283-98	Sequence 98, Appl
19	92	100.0	781	US-10-238-370-98	Sequence 98, Appl
20	92	100.0	781	US-10-245-055-98	Sequence 98, Appl
21	92	100.0	781	US-10-245-147-98	Sequence 98, Appl
22	92	100.0	781	US-10-245-730-98	Sequence 98, Appl
23	92	100.0	781	US-10-245-739-98	Sequence 98, Appl
24	92	100.0	781	US-10-246-210-98	Sequence 98, Appl
25	92	100.0	781	US-10-239-196-98	Sequence 98, Appl
26	92	100.0	781	US-10-243-024-98	Sequence 98, Appl
27	92	100.0	781	US-10-243-409-98	Sequence 98, Appl
28	92	100.0	781	US-10-245-621-98	Sequence 98, Appl
29	92	100.0	781	US-10-245-880-98	Sequence 98, Appl
30	92	100.0	781	US-10-245-033-98	Sequence 98, Appl
31	92	100.0	781	US-10-243-095-98	Sequence 98, Appl
32	92	100.0	781	US-10-245-185-98	Sequence 98, Appl
33	92	100.0	781	US-10-245-427-98	Sequence 98, Appl
34	92	100.0	781	US-10-245-473-98	Sequence 98, Appl
35	92	100.0	781	US-10-245-770-98	Sequence 98, Appl
36	92	100.0	781	US-10-245-877-98	Sequence 98, Appl
37	92	100.0	781	US-10-246-976-98	Sequence 98, Appl
38	92	100.0	781	US-10-243-320-98	Sequence 98, Appl
39	92	100.0	781	US-10-162-435-13	Sequence 13, Appl
40	92	100.0	781	US-10-242-743-98	Sequence 98, Appl
41	92	100.0	781	US-10-242-845-98	Sequence 98, Appl
42	92	100.0	781	US-10-237-636-98	Sequence 98, Appl
43	92	100.0	781	US-10-238-325-98	Sequence 98, Appl
44	92	100.0	781	US-10-238-346-98	Sequence 98, Appl
45	92	100.0	781	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-11
; Sequence 11, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiayun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dimauc, Radje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-11
Query Match 100.0%; Score 92; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SGSTVTVTLSDVNDNP 18
|||||

Db 1 SGGTIVTVTLSDVNDNPP 18

RESULT 2

US-09-788-051-12
Sequence 12, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-12

Query Match

Best Local Similarity 100.0%; Score 92; DB 10; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18

Db 1 SGGTIVTVTLSDVNDNPP 18

RESULT 3

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patutajan, Weera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 482
LENGTH: 493
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-482

Query Match

Best Local Similarity 100.0%; Score 92; DB 15; Length 493;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18

Db 240 SGGTIVTVTLSDVNDNPP 257

RESULT 4

US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kohnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258,951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 92; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 240 SGSTVTVTLSDVNDNPP 257

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dmanac, Radofe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: POLYNUCLEOTIDES
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 92; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 224 SGSTVTVTLSDVNDNPP 241

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dmanac, Radofe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: POLYNUCLEOTIDES
; FILE REFERENCE: HYS-38
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 92; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 240 SGSTVTVTLSDVNDNPP 257

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 92; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 240 SGSTVTVTLSDVNDNPP 257

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C6
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

```
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-752-98
```

```
Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SGGTIVTTLSDVNDNPP 18
Db      240 SGGTIVTTLSDVNDNPP 257
```

```
RESULT 9
US-10-245-859-98
/ Sequence 98, Application US/10245859
/ Publication NO. US20030064474A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Bong Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245,859
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
```

```
/ Remaining prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-859-98
```

```
Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SGGTIVTTLSDVNDNPP 18
Db      240 SGGTIVTTLSDVNDNPP 257
```

```
RESULT 10
US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication NO. US2003006878A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Bong Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C112
/ CURRENT APPLICATION NUMBER: US/10/245,103
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-103-98
```

```
Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SGGTIVTTLSDVNDNPP 18
Db      240 SGGTIVTTLSDVNDNPP 257
```



```

/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-771-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTVTVTLSDVNDNPP 18
Db      240 SGGSTVTVTLSDVNDNPP 257

RESULT 14
US-10-245-851-98
/ Sequence 98, Application US/10245851
/ Publication No. US20030068782A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gueney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245, 851
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98
```

```

/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTVTVTLSDVNDNPP 18
Db      240 SGGSTVTVTLSDVNDNPP 257

RESULT 15
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gueney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245, 883
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98
```

Wed Dec 8 11:46:22 2004

us-09-788-051-12.rapb

Page 7

Qy 1 SGSTTVTVTLSDVNDNP 18
| | | | | | | | | | | | | | | | | |
Db 240 SGSTTVTVTLSDVNDNP 257

Search completed: December 8, 2004, 11:34:29
Job time : 18.3932 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 2.1464 Seconds
(without alignments)

556,152 Million cell updates/sec

Title: US-09-788-051-12

Percent score: 92

Sequence: 1 SGSTVTVTLSVDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 segs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
5: /cgm2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgm2_6/ptodata/1/iaa/backfiller1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	90.2	109	3	US-09-187-859-17
2	83	90.2	109	4	US-09-839-542B-17
3	83	90.2	109	4	US-09-535-852-17
4	83	90.2	532	1	US-08-188-228-44
5	83	90.2	532	1	US-08-332-638-44
6	83	90.2	793	1	US-08-188-228-54
7	83	90.2	793	1	US-08-332-643-48
8	83	90.2	793	1	US-08-332-638-54
9	83	90.2	799	1	US-08-188-228-42
10	83	90.2	799	1	US-08-332-638-42
11	82	89.1	109	3	US-09-187-859-11
12	82	89.1	109	4	US-09-839-542B-11
13	82	89.1	109	4	US-09-535-852-11
14	80	87.0	109	3	US-09-187-859-8
15	80	87.0	109	3	US-09-187-859-8
16	80	87.0	109	4	US-09-839-542B-23
17	80	87.0	109	4	US-09-839-542B-23
18	80	87.0	109	4	US-09-535-852-8
19	80	87.0	109	4	US-09-535-852-23
20	80	87.0	653	1	US-08-188-228-46
21	80	87.0	653	1	US-08-332-638-46
22	79	85.9	109	3	US-09-187-859-5
23	79	85.9	109	4	US-09-839-542B-5
24	79	85.9	109	4	US-09-535-852-5
25	79	85.9	615	2	US-08-738-349-12
26	79	85.9	693	2	US-08-738-349-6
27	79	85.9	693	4	US-09-919-497-55

28	79	85.9	796	1	US-08-188-228-58	Sequence 58, Appl
29	79	85.9	796	1	US-08-332-643-52	Sequence 52, Appl
30	79	85.9	796	1	US-08-332-638-58	Sequence 58, Appl
31	79	85.9	796	2	US-08-738-348-2	Sequence 2, Appl
32	79	85.9	796	2	US-08-738-348-4	Sequence 4, Appl
33	79	85.9	796	4	US-09-654-328-2	Sequence 15, Appl
34	71	77.2	109	3	US-09-839-542B-15	Sequence 15, Appl
35	71	77.2	109	4	US-09-535-852-15	Sequence 15, Appl
36	71	77.2	794	1	US-08-188-228-60	Sequence 60, Appl
37	71	77.2	794	1	US-08-332-643-54	Sequence 54, Appl
38	71	77.2	794	1	US-08-332-638-60	Sequence 60, Appl
39	71	77.2	148	1	US-07-998-003A-36	Sequence 36, Appl
40	62	67.4	148	1	US-08-453-274B-36	Sequence 36, Appl
41	62	67.4	148	1	US-08-453-695A-36	Sequence 36, Appl
42	62	67.4	148	1	US-08-268-161A-36	Sequence 36, Appl
43	62	67.4	148	2	US-08-453-702A-36	Sequence 36, Appl
44	62	67.4	148	2	US-09-099-639-36	Sequence 36, Appl
45	62	67.4	148	3	US-09-099-639-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-187-859-17 Application US/09187859A
Sequence 17, Applicant: Blaschuk, Orest W.
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086, 407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-17

Query Match 90.2%; Score 83; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 16-05; 1; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy 1 SGSTVTVTLSVDVNDNP 18
Db 90 SGSTVTVTLSVDVNDNP 107

RESULT 2
US-09-839-542B-17 Application US/09839542B
Sequence 17, Applicant: Symonds, James Matthew
Patent No. 656996
GENERAL INFORMATION:
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086, 407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-839-542B-17

RESULT 4
 US-08-188-228-44
 ; Sequence 44, Application US/08188228
 ; Patent No. 3597725
 ;
 ; GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 ;
 ; COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188,228
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,460
 FILING DATE: 19 APR 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5597725and, Greta E.
 REGISTRATION NUMBER: 35,302

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,502
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match          90.2%   Score 83;   DB 1;   Length 532;
Best Local Similarity 83.3%   Pred. No. 6,7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
1 GSGTIVTVTLISNVNNDNP 1A

```


Db 257 SGTTLVTLTVDVNDNP 274

RESULT 6
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54
Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTTLVTLTSPVNDNP 18
Db 250 SGTTLVTLTVDVNDNP 267

RESULT 8
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro.
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48
Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTTLVTLTSPVNDNP 18
Db 250 SGTTLVTLTVDVNDNP 267

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
Db 250 SGTITLTVLTVDNDNP 267

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
Db 257 SGTITLTVLTVDNDNP 274

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
Db 257 SGTITLTVLTVDNDNP 274

RESULT 11
US-09-187-859-11
Sequence 11, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086, 407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-187-859-11

Query Match 89.1%; Score 82; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSGTIVTIVTLSDVNDNPP 18
DB 90 GGTIVTIVTLSDVNDNPP 107

RESULT 12
US-09-839-542B-11
Sequence 11, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-839-542B-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSGTIVTIVTLSDVNDNPP 18
DB 90 GGTIVTIVTLSDVNDNPP 107

RESULT 13
US-09-535-852-11
Sequence 11, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James M.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-535-852-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSGTIVTIVTLSDVNDNPP 18

DB 90 GGTIVTIVTLSDVNDNPP 107

RESULT 14
US-09-187-859-8
Sequence 8, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-8

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSGTIVTIVTLSDVNDNPP 18
DB 90 GGTIVTIVTLSDVNDNPP 107

RESULT 15
US-09-187-859-23
Sequence 23, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 109
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-187-859-23

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSGTIVTIVTLSDVNDNPP 18
DB 90 GGTIVTIVTLSDVNDNPP 107

Search completed: December 8, 2004, 10:01:14
Job time : 3.1464 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 3.88:94 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-13
Perfect score: 243
Sequence: 1 DVASRVAVQDAPEPPAFTQ.....ENKAPGLVQISADLDP 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	112	46.1	793	2	D38892
2	108	44.4	796	2	A38992
3	108	44.4	796	2	I48277
4	108	44.4	796	2	I49556
5	108	44.4	796	2	A53584
6	106	43.6	794	2	I59372
7	102	42.0	785	2	I50180
8	101	41.6	790	2	I37016
9	99	40.7	789	2	I52701
10	97.5	40.1	5147	1	IJFFTM
11	95	39.1	790	2	I50178
12	95	39.1	814	2	G02878
13	92	37.9	790	2	G02678
14	91	37.4	790	2	I51638
15	90.5	37.2	701	2	T17248
16	85.5	35.2	871	2	S47518
17	85.5	35.2	896	2	I45858
18	84.5	34.8	826	2	B55363
19	84.5	34.8	896	2	A53563
20	84.5	34.8	1072	2	T00041
21	81.5	33.5	784	1	IJHUC5
22	81.5	33.5	893	1	IJHUCD
23	81.5	33.5	863	1	IJHODC
24	80.5	33.1	1069	2	T00043
25	80.5	33.1	1544	2	T29482
26	80	32.9	847	1	IJHUDA
27	80	32.9	901	1	IJHUDA
28	79	32.5	770	2	B48910
29	79	32.5	824	2	A48910

30	79	32.5	840	2	I37281	Desla precursor -
31	79	32.5	894	2	I37282	Desla precursor -
32	79	32.5	2163	2	T15276	hypothetical prote
33	78.5	32.3	3097	2	T00021	DN-cadherin - frui
34	77.5	31.9	4351	2	T00252	MEG1 protein - fru
35	77	31.7	761	2	IJHODE	desmocollin 1a - b
36	77	31.7	839	1	IJBODF	desmocollin 1b pre
37	76	31.3	1200	2	T00042	BH-protocadherin p
38	75	30.9	827	2	A53954	Li-cadherin precurs
39	74.5	30.7	889	2	T09055	protocadherin 68 -
40	74.5	30.7	1180	2	T31066	vascular cadherin -
41	72.5	29.8	732	1	IJHOCB	B-cadherin precurs
42	72	29.6	730	1	IJHOCM	M-cadherin - mouse
43	71	29.2	877	1	IJHOCN	N-cadherin precurs
44	71	29.2	906	1	IJHUCN	cadherin 2 precurs
45	71	29.2	912	1	IJHUCN	N-cadherin precurs

ALIGNMENTS

RESULT 1
D38992
cadherin 8 - human
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence.revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305, MUID:91283540, PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:IJ34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
C:Genetics:
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 46.1%; Score 112; DB 2; Length 793;
Best local similarity 45.7%; Pred. No. 5.1e-05;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
DB 1 DVASRVAVQDAPEPPAFTQAAVHLTVENKAPGLVQISADLDP 46
367 DTAIVKIVEDADEPFPVSSPTVLEVHNAALNSVIGVTARDPD 412
RESULT 2
A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence.revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305, MUID:91283540, PMID:2059658
A:Accession: A38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: UNIPROT:P55287; GB:IJ34056; NID:G506403; PIDN:AAA35622.1; PID:G506404
C:Genetics:
A:Gene: GDB:CDH11; OB
A:Cross-references: GDB:512891; OMIM:600023
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology

C:\Accession: 150180 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1333, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: 150178; PMID:95309115; PMID:7540531
A/Accession: 150180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NAK>
A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
C/Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 42.0%; Score 102; DB 2; Length 785;
Best Local Similarity 38.3%; Pred. No. 9, 1e-05;
Matches 18; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFQAAVHLYTPENKAPGLTVGQISADDD 47
Db 360 DMTATVAVVDDVDEPVPFSLKAVIILQIRDAQINTTIGSVTAQDPDA 406

RESULT 8
137016
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: 137016
R/Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A>Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the f
A/Reference number: 137016; PMID:9562134; PMID:7743525
A/Accession: 137016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
C/Genetics:
A/Genes: GDB:CDH6
A/Cross-references: GDB:5622908
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 41.6%; Score 101; DB 2; Length 790;
Best Local Similarity 40.4%; Pred. No. 0.00012;
Matches 19; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFQAAVHLYTPENKAPGLTVGQISADDD 47
Db 366 DSATVAVVDDVDEPVPFSLKAVIILQIRDAQINTTIGSVTAQDPDA 412

RESULT 9
152701
K-cadherin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 152701
R/Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, T.
Cancer Res. 54, 3034-3041, 1994
A>Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A/Reference number: 152701; PMID:94243827; PMID:8187093
A/Accession: 152701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RES>
A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435461
C/Genetics:
A/Genes: KCAD
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 40.7%; Score 99; DB 2; Length 789;
Best Local Similarity 40.4%; Pred. No. 0.00022;

Matches 19; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
Qy 1 DVASVRVAVQDAPEPPAFQAAVHLYTPENKAPGLTVGQISADDD 47
Db 366 DSATVAVVDDVDEPVPFSLKAVIILQIRDAQINTTIGSVTAQDPDA 412

RESULT 10
1UFFFM
C/Superfamily: cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C/Accession: A41087; B41087
R/Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Blessmann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A>Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cad
A/Reference number: A41087; PMID:92069752; PMID:1959133
A/Accession: A41087
A/Molecule type: DNA
A/Residues: 1-142,487-1278 <MAH>
A/Cross-references: GB:M80537
A/Note: 1229-Gly and 1233-Ser were also found
C/Genetics:
A/Genes: fat
A/Cross-references: FlyBase:FBgn0001075
C/Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homolog
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:1-85/Domain: signal sequence #status predicted <SIG>
F:36-5147/Product: cadherin-related tumor suppressor #status predicted <EXT>
F:36-4583/Domain: extracellular #status predicted <EXT>
F:51-156/Domain: cadherin repeat homology <CR1>
F:159-270/Domain: cadherin repeat homology <CR2>
F:217-382/Domain: cadherin repeat homology <CR3>
F:320-494/Domain: cadherin repeat homology <CR4>
F:497-559/Domain: cadherin repeat homology <CR5>
F:602-708/Domain: cadherin repeat homology <CR6>
F:718-822/Domain: cadherin repeat homology <CR7>
F:831-942/Domain: cadherin repeat homology <CR8>
F:948-1049/Domain: cadherin repeat homology <CR9>
F:1052-1153/Domain: cadherin repeat homology <CR10>
F:1156-1278/Domain: cadherin repeat homology <CR11>
F:1281-1384/Domain: cadherin repeat homology <CR12>
F:1387-1489/Domain: cadherin repeat homology <CR13>
F:1492-1601/Domain: cadherin repeat homology <CR14>
F:1607-1713/Domain: cadherin repeat homology <CR15>
F:1717-1823/Domain: cadherin repeat homology <CR16>
F:1826-1922/Domain: cadherin repeat homology <CR17>
F:1925-2027/Domain: cadherin repeat homology <CR18>
F:2028-2167/Domain: cadherin repeat homology <CR19>
F:2169-2278/Domain: cadherin repeat homology <CR20>
F:2281-2384/Domain: cadherin repeat homology <CR21>
F:2387-2491/Domain: cadherin repeat homology <CR22>
F:2494-2596/Domain: cadherin repeat homology <CR23>
F:2599-2703/Domain: cadherin repeat homology <CR24>
F:2707-2810/Domain: cadherin repeat homology <CR25>
F:2813-2913/Domain: cadherin repeat homology <CR26>
F:2915-3013/Domain: cadherin repeat homology <CR27>
F:3014-3124/Domain: cadherin repeat homology <CR28>
F:3127-3229/Domain: cadherin repeat homology <CR29>
F:3232-3334/Domain: cadherin repeat homology <CR30>
F:3337-3439/Domain: cadherin repeat homology <CR31>
F:3442-3545/Domain: cadherin repeat homology <CR32>
F:3548-3651/Domain: cadherin repeat homology <CR33>
F:3654-3756/Domain: cadherin repeat homology <CR34>
F:3759-4010/Domain: EGF homology <EG1>
F:4017-4048/Domain: EGF homology <EG2>
F:4056-4089/Domain: EGF homology <EG3>
F:4096-4127/Domain: EGF homology <EG4>
F:4584-4609/Domain: transmembrane #status predicted <TM>

F,4610-5147/Domain: intracellular #status predicted <INT>

Query Match 40.1%; Score 97.5; DB 1; Length 5147;

Best Local Similarity 43.8%; Pred. No. 0.003; Mismatches 21; Indels 1; Gaps 1;

Matches 21; Conservative 5; Mismatches 21; Indels 1; Gaps 1;

Db 3317

RESULT 11

cadherin-6B - chicken

C/Species: Gallus gallus (chicken)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I50178

R/Nakagawa, S.; Takeichi, M.

Development 121, 1321-1332, 1995

A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A/Reference number: I50178; PMID:95309115; PMID:7540531

A/Accession: I50178

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <NA>

A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BAA07720.1; PID:9867998

A/Superfamily: cadherin; cadherin repeat homology

F,162-268/Domain: cadherin repeat homology <CDH>

Query Match 39.1%; Score 95; DB 2; Length 790;

Best Local Similarity 36.2%; Pred. No. 0.007; Mismatches 17; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Db 366

RESULT 12

cadherin-15 precursor - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C/Accession: G02878

R/Shimoyama, Y.

submitted to GenBank, February 1996

A/Reference number: H01775

A/Accession: G02878

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-814 <SH1>

A/Cross-references: UNIPROT:P55291; GB:D83542; NID:91208423; PIDN:BAA12012.1; PID:912084

C/Genetics:

A/Gene: GDB:CDH15; CDH14; CDH3

A/Cross-references: GDB:391031; OMIM:114019

A/Map position: 16q22.1-16q22.1

A/Superfamily: cadherin; cadherin repeat homology

F,1-17/Domain: signal sequence #status predicted <SIG>

F,155-260/Domain: cadherin repeat homology <CDH>

Query Match 39.1%; Score 95; DB 2; Length 814;

Best Local Similarity 46.7%; Pred. No. 0.00073; Mismatches 21; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Db 3

RESULT 13

G02678

cadherin-14 - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C/Accession: G02678

R/Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01584

A/Accession: G02678

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <SH1>

A/Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:91389652; PIDN:AAB02933.1; PID:913

A/Superfamily: cadherin; cadherin repeat homology

F,162-268/Domain: cadherin repeat homology <CDH>

Query Match 37.9%; Score 92; DB 2; Length 790;

Best Local Similarity 40.4%; Pred. No. 0.0017; Mismatches 19; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Db 366

RESULT 14

F-cadherin - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: I51638; S5391

R/Espebeth, A.; Johnson, E.; Kintner, C.

Mol. Cell. Neurosci. 6, 199-212, 1995

A/Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mol

A/Accession: I51638; PMID:96039533; PMID:7496627

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <ESP>

A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CAA59679.1; PID:9854

A/Superfamily: cadherin; cadherin repeat homology

F,161-267/Domain: cadherin repeat homology <CR2>

Query Match 37.4%; Score 91; DB 2; Length 790;

Best Local Similarity 40.4%; Pred. No. 0.0022; Mismatches 19; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Db 365

RESULT 15

hypothetical protein DKFP586B021.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T17243

R/Koehler, K.; Beyer, A.; Newes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A/Reference number: T17243

A/Accession: T17243

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-701 <KOE>

A/Cross-references: UNIPROT:Q9Y5E4; EMBL:AL117449

A/Experimental source: adult uterus; clone DKFP586B0217

C/Genetics:

A/Note: DKFP586B021.1

Query Match 37.2%; Score 90.5; DB 2; Length 701;

Best Local Similarity 44.4%; Pred. No. 0.0023; Mismatches 20; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

Db 4

RESULT 15

SVRAVAVODABE-PPAFQAAYHLTVPENKAPGTLVGQISAADLS 47

Wed Dec 8 11:46:24 2004

us-09-788-051-13.rpr

Page 5

Db 341 NITVLVSDVDNDNAPAFOTQSYTLFVRENNSPALHIGSVSATDRDS 385

Search completed: December 8, 2004, 10:27:08
Job time : 3.88194 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.2397 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243

Sequence: 1 DVASRVAVQDAPBPAPFTQ.....ENKAPGLVQGISADLDSF 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	100.0	370	086T00	086T00 homo sapien
2	243	100.0	493	096LQ7	096LQ7 homo sapien
3	243	100.0	819	CAD6_HUMAN	086T00 homo sapien
4	227	93.4	781	06PFX6	06PFX6 mus musculu
5	227	93.4	781	AAH57373	AAH57373 mus muscu
6	113	46.5	792	CAD6_CHICK	093119 gallus gall
7	112	46.1	508	06PAN4	06PAN4 mus musculu
8	112	46.1	508	AAH60200	AAH60200 mus muscu
9	112	46.1	519	090425	090425 brachydanio
10	112	46.1	716	08C375	08C375 mus musculu
11	112	46.1	716	08C449	08C449 mus musculu
12	112	46.1	716	AAH57581	AAH57581 mus muscu
13	112	46.1	754	08BRK4	08BRK4 mus musculu
14	112	46.1	799	CAD6_HUMAN	P55286 homo sapien
15	112	46.1	799	CAD6_MOUSE	P97291 mus musculu
16	112	46.1	799	CAD6_RAT	054600 rattus norv
17	111	45.7	796	096C29	096C29 homo sapien
18	109	44.9	789	CAD9_HUMAN	Q9UB44 homo sapien
19	108	44.4	796	CAD6_HUMAN	P55287 homo sapien
20	108	44.4	796	CAD6_MOUSE	P55288 mus musculu
21	108	44.4	796	08C706	08C706 mus musculu
22	106	43.6	794	CAD6_HUMAN	P55289 homo sapien
23	106	43.6	794	086UD2	086UD2 homo sapien
24	102	42.0	551	08AWW2	08AWW2 gallus gall
25	102	42.0	785	CAD7_CHICK	Q90763 gallus gall
26	102	42.0	794	093264	093264 xenopus lae
27	101.5	41.8	5147	FAT_DROME	P33450 drosophila
28	101	41.6	790	CAD6_HUMAN	P55285 homo sapien
29	99	40.7	789	CAD6_RAT	P55280 rattus norv
30	99	40.7	792	09DF80	09DF80 xenopus lae
31	99	40.7	792	09DF81	09DF81 xenopus lae

32	97.5	40.1	794	2	Q925L0	Q925L0 mus musculu
33	97.5	40.1	931	1	CDG3_HUMAN	Q9Y3H4 homo sapien
34	97	39.9	788	1	CAD6_HUMAN	Q9Y6B8 homo sapien
35	97	39.9	788	2	08CWS7	08CWS7 mus musculu
36	97	39.9	788	2	08VI68	08VI68 mus musculu
37	97	39.9	788	2	AAH62962	AAH62962 mus muscu
38	97	39.9	789	1	CAD6_CHICK	P79955 gallus gall
39	97	39.9	801	1	CAD6_HUMAN	Q9H6B6 homo sapien
40	95	39.1	790	1	CAD6_CHICK	Q90762 gallus gall
41	95	39.1	814	1	CAD6_HUMAN	P55291 homo sapien
42	94.5	38.9	794	2	08C8Z3	08C8Z3 mus musculu
43	94.5	38.9	794	2	09IXZ8	09IXZ8 mus musculu
44	93.5	38.5	787	1	CDBF_HUMAN	Q9Y3E8 homo sapien
45	93.5	38.5	829	2	Q8BN17	Q8BN17 mus musculu

ALIGNMENTS

RESULT 1	
Q96T00	PRELIMINARY; PRT; 370 AA.
AC Q96T00:	
DT 01-JUN-2003 (Tremblrel. 24, Created)	
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)	
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)	
DE Full-length cDNA clone CSODK003Y017 of Hela cells of Homo sapiens (human) (Fragment).	
DE Homo sapiens (Human).	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Hela cells;	
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	
CC -1- SIMILARITY: Contains 4 cadherin domains.	
EMBL: BX248303; CAD62630.1; -	
GO: GO:0016020; C:membrane; IEA.	
GO: GO:0005509; F:calcium ion binding; IEA.	
GO: GO:0007156; P:homophilic cell adhesion; IEA.	
InterPro: IPR002126; Cadherin.	
Pfam: PF00028; Cadherin; 3.	
PRINTS: PR00205; CADHERIN.	
SMART: SM00112; CA; 2	
PROSITE: PS00232; CADHERIN_1; 1.	
PROSITE: PS0268; CADHERIN_2; 4.	
KW Calcium; Calcium-binding.	
FT NON TER 1	
FT NON TER 370	
SEQUENCE 370 AA; 39479 MW; 3996D4AF8A4500E0 CRC64;	
Query Match 100.0%; Score 243; DB 2; Length 370;	
Best Local Similarity 100.0%; Pred. No. 1.2e-20;	
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 DVASRVAVQDAPBPAPFTQAAYLTVENKAPGLVQGISADLDSF 48	
DB 118 DVASRVAVQDAPBPAPFTQAAYLTVENKAPGLVQGISADLDSF 165	
RESULT 2	
Q96LQ7	PRELIMINARY; PRT; 493 AA.
AC Q96LQ7:	
DT 01-DEC-2001 (Tremblrel. 19, Created)	
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)	

DE 01-OCT-2003 (TriEMBL-rel. 25, Last annotation update)

DT Hypoetical protein FLJ25133.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RC TISSUE=Thyroid;
RA Nitomiyu K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: Contains 4 cadherin domains.
DR EMBL; AK057922; BAB71613.1; --
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPRO02126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM0112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
KW Calcium; Cys502-binding
SQ SEQUENCE 493 AA; 53616 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 243; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.ee-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Ct 1 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 48
357 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 404
|||||

RESULT 3
CADO_HUMAN STANDARD; PRT; 819 AA.
ID _CADO_HUMAN STANDARD; PRT; 819 AA.
AC ORGUP0; ORGUP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNC2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RC TISSUE=Thyroid;
RA Nitomiyu K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: Contains 4 cadherin domains.
DR EMBL; AK057922; BAB71613.1; --
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPRO02126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM0112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
KW Calcium; Cys502-binding
SQ SEQUENCE 493 AA; 53616 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 243; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.ee-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Ct 1 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 48
357 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 404
|||||

RESULT 3
CADO_HUMAN STANDARD; PRT; 819 AA.
ID _CADO_HUMAN STANDARD; PRT; 819 AA.
AC ORGUP0; ORGUP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNC2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RC TISSUE=Thyroid;
RA Nitomiyu K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: Contains 4 cadherin domains.
DR EMBL; AK057922; BAB71613.1; --
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPRO02126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM0112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
KW Calcium; Cys502-binding
SQ SEQUENCE 493 AA; 53616 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 243; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.ee-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Ct 1 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 48
357 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 404
|||||

RESULT 3
CADO_HUMAN STANDARD; PRT; 819 AA.
ID _CADO_HUMAN STANDARD; PRT; 819 AA.
AC ORGUP0; ORGUP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNC2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RC TISSUE=Thyroid;
RA Nitomiyu K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: Contains 4 cadherin domains.
DR EMBL; AK057922; BAB71613.1; --
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPRO02126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM0112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
KW Calcium; Cys502-binding
SQ SEQUENCE 493 AA; 53616 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 243; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.ee-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Ct 1 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 48
357 DVASVAVAVQDAPPEPAPFOAAYHETVGENKAPGTWVGQISADLSP 404
|||||

RESULT 3
CADO_HUMAN STANDARD; PRT; 819 AA.
ID _CADO_HUMAN STANDARD; PRT; 819 AA.
AC ORGUP0; ORGUP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNC2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RC TISSUE=Thyroid;
RA Nitomiyu K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishik

RA	Goodowski J., Gray A.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale
RL	effort to identify novel human secreted and transmembrane proteins: a
RN	Bioinformatics assessment.";
RP	Genome Res. 13:2265-2270(2003).
RC	[3]
RD	SEQUENCE FROM N.A. (ISOFORM 3).
RE	TISSUE=Testis;
RF	Blum F., Battersachs S., Mewes H.-W., Gaessenhuber J., Wiemann S.;
RG	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RH	- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
RI	They preferentially interact with themselves in a homophilic
RJ	manner in connecting cells; cadherins may thus contribute to the
RK	sorting of heterogeneous cell types. Cadherin-24 mediate strong
RL	cell-cell adhesion.
RM	- SUBUNIT: Associates with alpha-, beta- and delta-catennins.
RN	- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
RO	- ALTERNATIVE PRODUCTS:
RP	Event=Alternative splicing; Named isoforms=3;
RQ	Name=1; Synonyms=Long form;
RS	IsoId=Q86UP0-1; Sequence=DsDisplayed;
RT	Name=2; Synonyms=Short form;
RU	IsoId=Q86UP0-2; Sequence=VSP_008717;
RV	Name=3;
RW	IsoId=Q86UP0-3; Sequence=VSP_008718; VSP_008719;
RX	Note=No experimental confirmation available;
RY	- SIMILARITY: Contains 5 cadherin domains.
RZ	-----
SA	This SWISS-PROT entry is copyright. It is produced through a collaboration
SB	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
SC	the European Bioinformatics Institute. There are no restrictions on its
SD	use by non-profit institutions as long as its content is in no way
SE	modified and this statement is not removed. Usage by and for commercial
SF	entities requires a license agreement (See http://www.isb-sib.ch/announce/
SG	or send an email to license@isb-sib.ch).
SH	-----
SI	EMBL; AY260900; AA220580.1; .
SJ	EMBL; AY260901; AAP20591.1; .
SK	EMBL; AY358199; AAQ85566.1; .
SL	EMBL; AL137477; CAB70758.1; .
SM	PIR; T46418; T46418.
SN	HSSP; P09803; I17M.
SO	GeneW; HGNC:14265; CDR24.
SP	InferPro; IPRO0126; Cadherin.
SQ	InferPro; IPRO0123; Cadherin_C_term.
SR	InterPro; IPRO0123; Cadherin_C_term.
ST	Pfam; PF01049; Cadherin_5.
SV	Pfam; PF01049; Cadherin_C_1.
SW	PRINTS; PR00205; CADHERIN.
SX	PROSITE; PS00232; CADHERIN.
SY	PROSITE; PS50268; CADHERIN_2; 5.
SZ	KM Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
TA	Multigene family; Repeat; Signal; Transmembrane.
TB	KW SIGNAL
TC	FT PROPEP 1 19
TD	FT CHAIN 21 44
TE	FT DOMAIN 45 819
TF	FT TRANSSEM 642 662
TG	FT DOMAIN 663 819
TH	FT DOMAIN 46 150
TI	FT DOMAIN 151 259
TJ	FT DOMAIN 260 374
TK	FT DOMAIN 375 517
TL	FT DOMAIN 517 630
TM	CARBOHYD 446 446
TN	CARBOHYD 548 548
TO	CARBOHYD 563 563
TP	VARSPIC 455 492
TR	VARSPIC 1 427
TS	VARSPIC 428 492
TT	EGTHTPAADPRAPAKAHNTLTATLGMSWGPERGWPLL
TV	VAVMSAAPPPSPVSAGVGIPQ -> KNIVCTWSYHS
TW	ALTFSTCIHAVMCFCLMLVASCGIHAHPHLRNVCWC

FT VNRVCGVLPs (in isoform 3).
 FT /FTIR-VSP 008719.
 SQ SEQUENCE 819 AA; 87751 MW; 9083034F18BA7E4A CRC64;
 Query Match 100.0%; Score 243; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 2.7e-20;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 404

RESULT 4
 ID PRELIMINARY; PRT; 781 AA.
 AC Q6PX6;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF000028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 93.4%; Score 227; DB 2; Length 781;
 Best Local Similarity 91.7%; Pred. No. 2.1e-18;
 Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 404

RESULT 5
 ID PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057373; AAH57373.1; -
 SO SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 93.4%; Score 227; DB 2; Length 781;
 Best Local Similarity 91.7%; Pred. No. 2.1e-18;
 Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLYTPENKAPGTLVGOISADLDSF 404

RESULT 6
 ID CADB CHICK STANDARD; PRT; 792 AA.
 AC O93319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Kotliarsky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF055342; AAC3675.1; -
 DR HSSP; P09803; 117W.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002123; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSMEM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3486C6868731A9 CRC64;
 Query Match 46.5%; Score 113; DB 1; Length 792;
 Best Local Similarity 44.7%; Pred. No. 9.1e-05;
 Matches 21; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEAKAPGTLVQGISAAADLS 47
 DB 366 DLTATKIVEDDEPVLKPSYIFPEVQENASGTVGKHAQKDPDA 412
 RESULT 7
 O6PAN4 PRELIMINARY; PRT; 508 AA.
 ID O6PAN4
 AC O6PAN4
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Matulis N.A., Farnier A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whitting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin_4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 DR KX Calcium-binding.
 KW SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;
 Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEAKAPGTLVQGISAAADLS 46
 DB 374 DLTATKIVEDDEPVLKPSYIFPEVQENASGTVGKHAQKDPDA 419
 RESULT 8
 AAH60200 PRELIMINARY; PRT; 508 AA.
 ID AAH60200
 AC AAH60200
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Matulis N.A., Farnier A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whitting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin_4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 DR KX Calcium-binding.
 KW SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliathy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bonfield G.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skitwood U., Schmutz U., Myers R.W., Butterfield Y.S.,
 RA Krzywincki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC060200; AAH60200.1; -
 SQ SEQUENCE 508 AA, 56388 MW, 9053F774BCF52255 CRC64;

Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASRVAVODAPPEPFTQAAYHLTVPENKAPGTLVGQISADLD 46
 Db 374 DTTIVKISVEDADEPFPFMAFSYNFVEVENAPAGTLVGRVHADTD 119

RESULT 9
 ID 090425 PRELIMINARY; PRT; 519 AA.
 AC 090425;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Ventral neural cadherin (Fragment).
 GN Namescdh1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96363857; PubMed=8725279;
 RA Franklin U.I., Sargent T.D.,
 RT "Ventral neural cadherin, a novel cadherin expressed in a subset of
 RT neural tissues in the zebrafish embryo.";
 RL Dev. Dyn. 206:121-130(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Franklin J.L.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 3 cadherin domains.
 DR EMBL: U01419; AAB47406.1; -
 DR HSSP: P09803; 117M
 DR ZFIN: ZDB-GENE-980526-170; cdh11.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_3.
 DR Pfam: PF01049; Cadherin_C1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 3.
 DR PROSITE: PS00232; CADHERIN_1; 1.
 DR PROSITE: PS50268; CADHERIN_2; 3.

KW Calcium-binding; Cell adhesion; Transmembrane.
 FT NON TER 1
 SQ SEQUENCE 519 AA; 57807 MW; 0D2547C30D46B28 CRC64;

Query Match 46.1%; Score 112; DB 2; Length 519;
 Best Local Similarity 45.7%; Pred. No. 7.7e-05;
 Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 DVASRVAVODAPPEPFTQAAYHLTVPENKAPGTLVGQISADLD 46
 Db 93 DTTIVKISVEDADEPFPFMAFSYNFVEVENAPAGTLVGRVHADTD 138

RESULT 10
 ID 08C375 PRELIMINARY; PRT; 716 AA.
 AC 08C375;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone:D930046M17 product:cadherin 8, full insert
 DE sequence.
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishime T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).

RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kondo M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 CC - FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC - SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC - SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK086711; BAC39724.1; -.
 DR HSSP: P15116; INCU.
 DR MGD: MGI:107434; Cdh8.
 DR GO: GO:0016020; C-membrane; IEA.
 DR GO: GO:0005509; P-calcium ion binding; IEA.
 DR GO: GO:0007156; P-phospholipid cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PRO0205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00332; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79149 MW; 58BD598F638624A CRC64;

 Query Match 46.1%; Score 112; DB 2; Length 716;
 Best Local Similarity 45.7%; Pred. No. 0.00011;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

 QY 1 DVASRVAVQDAPEPPATQAAYHLTVENKAPGTLVQISADLD 46
 DB 374 DPAATKIVDEADPEPPVSPFYLLVEHNAALNSVIGQVARDPD 419

 RESULT 11
 Q8C449 PRELIMINARY; PRT; 716 AA.
 AC Q8C449;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus CDNA, RIKEN full-length enriched
 DE library, clone:CG3002D14 product:cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=99279253; PubMed=10345636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kondo H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kondo M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.A., Longellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyc S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeburg R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.U., Maiz M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.


```
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AK083092; BAC38758.1; -.
DR EMBL: BC057581; AAH57581.1; -.
DR HSSP: P5116; INCI.
DR MGD: MGI:107434; Cdh8.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PRO0205; CADHERIN.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.
KM SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 46.1%; Score 112; DB 2; Length 716;
Best Local Similarity 45.7%; Pred. No. 0.00011;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASVAVQDAPEPPAFTQAAYHLTPENKAGCTIVGOISADLD 46
DB 374 DTAIVKIVEDADEPVPFSSPTLYLEVHENAALNSVIGQVTAARDP 419

RESULT 12
AAH57581 PRELIMINARY; PRT; 716 AA.
AC AAH57581;
DT 01-MAR-2003 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477032;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schlier G.D.;
RA Altschul S.F.; Zeeberg B.; Buerger K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udell T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loggellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McMan P.J.; McKernan K.J.; Malek J.A.; Gunnarsson P.H.;
RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahney J.; Helton E.; Kettman W.; Madan A.; Rodrigues S.; Sanchez A.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Kravinsky M.I.; Skalska U.; Smalins D.E.; Schmeich A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBD databases.

DR EMBL: BC057581; AAH57581.1; -.
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 46.1%; Score 112; DB 2; Length 716;
Best Local Similarity 45.7%; Pred. No. 0.00011;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASVAVQDAPEPPAFTQAAYHLTPENKAGCTIVGOISADLD 46
DB 374 DTAIVKIVEDADEPVPFSSPTLYLEVHENAALNSVIGQVTAARDP 419

RESULT 13
QBRK4 PRELIMINARY; PRT; 754 AA.
AC QBRK4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830083P13 product:cadherin 8, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cortex;
RC MEDLINE=99279253; PubMed=10349636;
RX Carninci P.; Hayashizaki Y.;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cortex;
RA The FANTOM Consortium;
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoaka S.; Sasaki N.; Carninci P.;
RA Kono H.; Akiyama J.; Nishi K.; Kitanai T.; Tashiro H.; Itoh M.;
RA Suni N.; Ishii Y.; Nakamura S.; Hazama M.; Nishite T.; Harada A.;
RA Yamamoto R.; Matsunoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA Fujiwaka S.; Inoue K.; Ozawa Y.; Izawa M.; Obara E.; Watanaka M.;
RA Okazaki Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsumura S.; Kawai J.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
```

RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo H., Kondo M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Mizuta M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takehashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK04046; BAC31751.1; -.
 DR HSSP: P5116; INCT.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005029; F:calcium ion binding; IEA.
 DR GO: GO:0007156; F:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR KEGG: K04060; Calcium-binding, Cell adhesion, Transmembrane.
 SC SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;
 Query Match Best Local Similarity 45.1%; Score 112; DB 2; Length 754;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASVAVAVQDAPEPAFTQAAVHLTVENKAPGTLVQGISADLD 46
 DB 374 DRAVAVIVEDADEPVPFSSPTLVLEVENNALNSVIGVATARDP 419
 RESULT 14
 CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitajima M., Nakori M.,
 RA "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins."
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Heilmann R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]

RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL: AB035305; BA87419.1; -.
 DR EMBL: L34060; AAA35628.1; ALT_INIT.
 DR HSSP: P09803; 117W.
 DR Genew: HGNC:1767; CDH8.
 DR MIM: 603008; -.
 DR GO: GO:0007155; F:cell adhesion; TAS.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR KEGG: K04060; Calcium-binding, Cell adhesion, Glycoprotein, Repeat, Signal;
 KW Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 62 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;
 Query Match Best Local Similarity 45.1%; Score 112; DB 1; Length 799;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASVAVAVQDAPEPAFTQAAVHLTVENKAPGTLVQGISADLD 46
 DB 374 DRAVAVIVEDADEPVPFSSPTLVLEVENNALNSVIGVATARDP 419
 RESULT 15
 CAD8 MOUSE

Search completed: December 8, 2004, 10:24:40
 Job time : 20.2397 secs

```

ID  CAD8_MOUSE      STANDARD;      PRT;      799 AA.
AC  P97231;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Cadherin-8 precursor.
GN  Name=Cdh8;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Swiss Webster / NIH;
RX  MEDLINE=97174321; PubMed=9022055;
RA  Korematu K., Redies C.;
RT  "Restricted expression of cadherin-8 in segmental and functional
RL  subdivisions of the embryonic mouse brain.";
CC  Dev. Dyn. 208:178-189(1997).
CC  -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC  They preferentially interact with themselves in a homophilic
CC  manner in connecting cells; cadherins may thus contribute to the
CC  sorting of heterogeneous cell types.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: Contains 5 cadherin domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X85600; CAA64857.1; -.
DR  HSSP; P09803; 117W.
DR  MGD; MG1:107434; Cdh8.
DR  InterPro; IPR002126; Cadherin.
DR  InterPro; IPR000233; Cadherin_C_term.
DR  Pfam; PF00028; Cadherin; 5.
DR  Pfam; PF01049; Cadherin_C; 1.
DR  PRINTS; PR00205; CADHERIN.
DR  SMART; SM00112; CA; 5.
DR  PROSITE; PS00232; CADHERIN_1; 3.
DR  PROSITE; PS50268; CADHERIN_2; 5.
KW  Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW  Transmembrane.
FT  SIGNAL          1      29      Potential.
FT  PROPEP          30      61      Potential.
FT  CHAIN           62      799      Cadherin-8.
FT  DOMAIN          62      621      Extracellular (Potential).
FT  TRANSMEM        622      642      Potential.
FT  TRANSMEM        643      799      Cytoplasmic (Potential).
FT  DOMAIN          62      167      Cadherin 1.
FT  DOMAIN          168      276      Cadherin 2.
FT  DOMAIN          277      391      Cadherin 3.
FT  DOMAIN          392      494      Cadherin 4.
FT  DOMAIN          495      616      Cadherin 5.
FT  CARBOHYD        188      188      N-linked (GlcNAc...) (Potential).
FT  CARBOHYD        463      463      N-linked (GlcNAc...) (Potential).
FT  CARBOHYD        473      473      N-linked (GlcNAc...) (Potential).
FT  CARBOHYD        544      544      N-linked (GlcNAc...) (Potential).
SQ  SEQUENCE        799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

```

Query Match 46.1%; Score 112; DB 1; Length 799;
 Best Local Similarity 45.7%; Pred. No. 0.00012;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 1 DVASVAVADAPAPPTQAAVHLTPENKAPGTLVQGISAADLD 46
 DB 374 DTAIVKIVEDADEPVPFSSPTLLLEVENAALNSVIGVYARDPD 419

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-13
Perfect score: 243
Sequence: 1 DVASRYVAVQDAPEPPAFTQ.....ENKAFGLVGOISADLSDP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358723299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.23sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	243	100.0	48	ADD29454 Human cad
2	243	100.0	193	ADD29456 Human cad
3	243	100.0	493	AD116946 Human NOV
4	243	100.0	607	ABBS3295 Human cad
5	243	100.0	620	ADD29448 Human cad
6	243	100.0	636	ADD29445 Human cad
7	243	100.0	781	ABBS3296 Human pol
8	243	100.0	781	AAW48736 Human cad
9	243	100.0	781	ABG34078 Human PRO
10	243	100.0	781	AD116604 Human NOV
11	243	100.0	781	AD116606 Human NOV
12	243	100.0	781	ABR40114 Human cel
13	243	100.0	781	ADA01356 Human PRO
14	243	100.0	781	ADA43795 Human sec
15	243	100.0	781	ADA43563 Human sec
16	243	100.0	781	ADA01238 Human PRO
17	243	100.0	781	ADA01122 Human sec
18	243	100.0	781	ADA43679 Human sec
19	243	100.0	781	ADA06941 Human PRO
20	243	100.0	781	ADA08439 Novel hum
21	243	100.0	781	ADB89722 Human PRO
22	243	100.0	781	ADB87005 Human PRO
23	243	100.0	781	ADB66160 Human sec
24	243	100.0	781	ADB89838 Human PRO
25	243	100.0	781	ADB99493 Novel hum

26	243	100.0	781	7	ADB66044
27	243	100.0	781	7	ADC23442
28	243	100.0	781	7	ADC26135
29	243	100.0	781	7	ADB04962
30	243	100.0	781	7	ADBE1268
31	243	100.0	781	7	ADBE8199
32	243	100.0	781	7	ADDS5494
33	243	100.0	781	7	ADBE6424
34	243	100.0	781	7	ADBE8199
35	243	100.0	781	7	ADBE8315
36	243	100.0	781	7	ADD90896
37	243	100.0	781	7	ADFP9451
38	243	100.0	781	7	ADG06544
39	243	100.0	781	7	ADG05495
40	243	100.0	781	7	ADG82496
41	243	100.0	781	8	ADE51749
42	243	100.0	781	8	ADE51865
43	243	100.0	781	8	ADE37723
44	243	100.0	781	8	ADE37607
45	243	100.0	781	8	ADD95378

ALIGNMENTS

RESULT 1
ADD29454
ID ADD29454 standard; protein; 48 AA.
XX
AC ADD29454;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID13.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytoskeletal; osteopetrotic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GODB/) GODBOLE S D.
PA (KUCO/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YRUN/) YRUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
PI Liu C, Drmanac RT;
XX
PI WPI, 2003-829799/77.
XX
DR Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 13; 63bp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytosolic or osteopetrotic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancer, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of a peptide fragment of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

XX
XX Sequence 48 AA;

Query Match 100.0%; Score 243; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQISADIDSP 48
DB 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQISADIDSP 48

RESULT 2

ID ADI16946 standard; protein, 193 AA.

XX
XX AC ADI16946;

DT 15-APR-2004 (first entry)

XX
XX DE Human cadherin-like protein peptide fragment Seq ID15.

XX
XX KW cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopetrotic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

XX
XX OS Homo sapiens.

XX
XX PN US200314491-A1.

XX
XX PD 31-JUL-2003.

XX
XX PF 16-FEB-2001; 2001US-00788051.

XX
XX PR 03-FEB-2000; 2000US-00469914.

XX
XX PR 27-APR-2000; 2000US-00560875.

XX
XX PA (GODB/) GODBOLE S D.

XX
XX PA (KUC/) KUO C.

XX
XX PA (ARTE/) ARTERBURN M C.

XX
XX PA (YUNG/) YUNG G.

XX
XX PA (PALE/) PALENCIA S.

XX
XX PA (TANG/) TANG Y T.

XX
XX PA (LUC/) LIU C.

XX
XX PA (DRMA/) DRMANAC R T.

XX
XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

XX
XX PI Liu C, Drmanac RT;

XX
XX DR WPI; 2003-829793/77.

XX
XX DR N-PSDB; ADD29460.

XX
XX PT Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancer, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.

XX
XX PS Claim 11; SEQ ID NO 15; 63bp; English.

XX
XX CC This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of
XX transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytosolic or osteopetrotic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancer, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of a peptide fragment of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

XX
XX Sequence 193 AA;

Query Match 100.0%; Score 243; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQISADIDSP 48
DB 96 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQISADIDSP 143

RESULT 3

ID ADI16946 standard; protein, 493 AA.

XX
XX AC ADI16946;

DT 15-APR-2004 (first entry)

XX
XX DE Human NOVX protein homologue SeqID 482.

XX
XX KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; str.

XX
XX OS Homo sapiens.

XX
XX PN WO200268649-A2.

XX
XX PD 06-SEP-2002.

XX
XX PF 31-JAN-2002; 2002WO-US002785.

XX
XX PR 31-JAN-2001; 2001US-0265395P.

XX
XX PR 31-JAN-2001; 2001US-0265412P.

XX
XX PR 31-JAN-2001; 2001US-0265514P.

XX
XX PR 31-JAN-2001; 2001US-0265517P.

XX
XX PR 02-FEB-2001; 2001US-0266406P.

XX
XX PR 05-FEB-2001; 2001US-0266767P.

XX
XX PR 07-FEB-2001; 2001US-0266775P.

XX
XX PR 08-FEB-2001; 2001US-0267057P.

XX
XX PR 09-FEB-2001; 2001US-0267459P.

XX
XX PR 15-FEB-2001; 2001US-0267823P.

XX
XX PR 26-FEB-2001; 2001US-0268974P.

XX
XX PR 27-FEB-2001; 2001US-0271839P.

XX
XX PR 27-FEB-2001; 2001US-0271835P.

XX
XX PR 02-MAR-2001; 2001US-0272788P.

XX
XX PR 14-MAR-2001; 2001US-0273046P.

XX
XX PR 14-MAR-2001; 2001US-0275942P.

XX
XX PR 14-MAR-2001; 2001US-0275947P.

XX
XX PR 14-MAR-2001; 2001US-0275989P.

XX
XX PR 15-MAR-2001; 2001US-0276448P.

XX
XX PR 15-MAR-2001; 2001US-0276450P.

XX
XX PR 16-MAR-2001; 2001US-0276397P.

XX
XX PR 16-MAR-2001; 2001US-0276768P.

XX
XX PR 20-MAR-2001; 2001US-0278652P.

XX
XX PR 26-MAR-2001; 2001US-0278775P.

XX
XX PR 26-MAR-2001; 2001US-0278778P.

PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312820P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 12-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 (CUBA-) CUBAGEN CORP.
 PI Tchernev VT, Spytek KA, Zerhusen BD, Paturajan M, Shinkets RA;
 PI Li L, Gangoli EA, Padgug M, Anderson DW, Rastelli L, Miller CE;
 PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
 PI Furek K, Groese WM, Alschbrook JP, Lepley DM, Rieger DK, Burgess CE;
 DR WPI, 2002-706998/76.
 XX New NOXV polypeptides and nucleic acids, useful for preventing or
 PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy, or
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 XX Disclosure, SEQ ID NO 482; 1498bp; English.
 XX
 XX This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOXV proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOXV polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, candidant, antiinflammatory, immunosuppressive, anti-allergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antistimatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, viricide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
 CC of the invention.
 XX
 XX Sequence 493 AA:
 SQ

Query Match 100.0%; Score 243; DB 5; Length 493;
 Best Local Similarity 100.0%; Pred. No. 6,7e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVASRVAVODAPEPPAFQTQAAVHLTPENKAGTIVGQISADLDSF 48
 DB 357 DVASRVAVODAPEPPAFQTQAAVHLTPENKAGTIVGQISADLDSF 404
 RESULT 4
 ABB53295
 ID ABB53295 standard; protein; 607 AA.
 XX
 AC ABB53295;
 DT 12-FEB-2002 (first entry)
 XX
 DE Human polypeptide #35.
 XX
 KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquiliser; antiarthritic; cardiant; antidiabetic;
 KW antiinflammatory; antipileptic; hepatotropic; viricide; antistimatic;
 KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.
 XX
 OS Homo sapiens.
 XX
 FN WC200181363-A1.
 XX
 PD 01-NOV-2001.
 XX
 PF 26-APR-2001; 2001WO-US013360.
 XX
 PR 27-APR-2000; 2000US-0199963P.
 PR 11-MAY-2000; 2000US-020336P.
 PR 25-MAY-2000; 2000US-0207087P.
 PR 26-MAY-2000; 2000US-0207546P.
 XX
 XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 XX
 XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lai Y, Xie Q;
 XX WPI; 2002-041392/05.
 DR N-PSDB; ABA90360.
 XX
 XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX
 XX Claim 1; Page 106-108; 116bp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 581, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 781, 662, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraspranuclear palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Bulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including

CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX SQ Sequence 607 AA;

Query Match 100.0%; Score 243; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 8.5e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVAVAVQADAPPPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 48
 |||||
 Db 357 DVASVAVAVQADAPPPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 404

RESULT 5

ADD29448
 ID ADD29448 standard; protein; 620 AA.

XX AC ADD29448;

XX DT 15-JAN-2004 (first entry)

XX DE Human cadherin-like mature protein.

XX KW cadherin-like protein; transmembrane protein; cadherin domain;

XX KM homotypic cell-cell adhesion; cytotatic; osteopathic; cancer;

XX KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KM metastatic tumour; human.

XX OS Homo sapiens.

XX PN US2003144491-A1.

XX PD 31-JUL-2003.

XX PF 16-FEB-2001; 2001US-00788051.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PA (GDB/) GODBOLE S D.

XX PA (KLOC/) KUO C.

XX PA (ARTE/) ARTERBURN M C.

XX PA (YEUN/) YEUNG G.

XX PA (PALE/) PALENCIA S.

XX PA (TANG/) TANG Y T.

XX PA (LITC/) LIT C.

XX PA (DRMA/) DRMANAC R T.

XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

XX PI Liu C, Drmanac RT;

XX DR WPI; 2003-829799/77.

XX PT Novel isolated human secreted cadherin-like polypeptide useful for

XX PT treating diseases such as cancers, osteoporosis, Paget's disease,

XX PT osteomalacia, hyperostosis, osteopetrosis.

XX PS Claim 11; SEQ ID NO 7; 63pp; English.

CC This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic

CC tumours. The present sequence is that of the mature human secreted
 CC cadherin-like protein which was used during the exemplification of the
 CC invention.

XX SQ Sequence 620 AA;

Query Match 100.0%; Score 243; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 8.7e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVAVAVQADAPPPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 48
 |||||
 Db 341 DVASVAVAVQADAPPPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 388

RESULT 6

ADD29445
 ID ADD29445 standard; protein; 636 AA.

XX AC ADD29445;

XX DT 15-JAN-2004 (first entry)

XX DE Human cadherin-like protein amino acid sequence.

XX KW cadherin-like protein; transmembrane protein; cadherin domain;

XX KM homotypic cell-cell adhesion; cytotatic; osteopathic; cancer;

XX KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KM metastatic tumour; human.

XX OS Homo sapiens.

XX PN US2003144491-A1.

XX PD 31-JUL-2003.

XX PF 16-FEB-2001; 2001US-00788051.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PA (GDB/) GODBOLE S D.

XX PA (KLOC/) KUO C.

XX PA (ARTE/) ARTERBURN M C.

XX PA (YEUN/) YEUNG G.

XX PA (PALE/) PALENCIA S.

XX PA (TANG/) TANG Y T.

XX PA (LITC/) LIT C.

XX PA (DRMA/) DRMANAC R T.

XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

XX PI Liu C, Drmanac RT;

XX DR WPI; 2003-829799/77.

XX PT Novel isolated human secreted cadherin-like polypeptide useful for

XX PT treating diseases such as cancers, osteoporosis, Paget's disease,

XX PT osteomalacia, hyperostosis, osteopetrosis.

XX PS Claim 11; SEQ ID NO 4; 63pp; English.

CC This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteoparathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

XX Sequence 636 AA;

SO Query Match 100.0%; Score 243; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 9e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSP 48
DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSP 404

RESULT 7
ABBS3296
ID ABBS3296 standard; protein; 781 AA.

XX AC ABBS3296;

DT 12-FEB-2002 (first entry)

XX Human polypeptide #36.

XX Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiac; antiautismic;
XX antiinflammatory; antihypertensive; hepatotropic; virotoxic; antidiabetic;
XX nephrotoxic; anorectic; cyostatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

PN WO200181363-A1.

XX 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-020336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS,

PI Lai Y, Xie Q;

XX WPI; 2002-041392/05.

DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

PT and treating diseases associated the polypeptide, e.g. Alzheimer's

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesiae.

XX Claim 1; Page 108-109; 116pp; English.

CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymphocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

SO Query Match 100.0%; Score 243; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSP 48
DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSP 404

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

XX AC AAM48736;

DT 28-MAR-2002 (first entry)

XX Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarrhythmic; antipneumatic;
XX dermatological; immunosuppressive; antiinflammatory; antiparatic;
XX antiautismic; antiallergic; antileptotic; haemostatic; antiparatic;
XX antithyroid; hypotensive; antiatherosclerotic; cardiac; antiarrhythmic;
XX anorectic; immunomodulatory; vasotropic; virotoxic; cyostatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.

XX Homo sapiens.

PN WO200190145-A2.

XX 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

XX (MTLL-) MILLENNIUM PHARM INC.

PA Curtis RAJ;

XX WPI; 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for

PT diagnosing and treating disorders e.g. obstructive jaundice, multiple

PT sclerosis, encephalomyelitis and atherosclerosis and to identify

XX modulators of therapeutic use.

XX Claim 9; Page 105; 119pp; English.

Query Match	100.0%	Score 243	DB 5	Length 781
Best Local Similarity	100.0%	Pred. No. 1,le-23		
Matches	48	Conservative	0	Mismatches 0; Indels 0; Gaps 0

QY	1	DVASVAVAVQDAPEPPAFITQAAYIHLTVENKAPGTLVQIQISADALDSD	48
Db	357	DVASVAVAVQDAPEPPAFITQAAYIHLTVENKAPGTLVQIQISADALDSD	404

RESULT 9	ABG34078	ABG34078 standard; protein; 781 AA.
ID	ABG34078	
AC	ABG34078;	
XX		
DT	15-JUL-2002 (First entry)	
XX		
DE	Human Pro peptide #49.	
XX		
KW	Human; PRO; secreted protein; transmembrane protein; genetic disorder; tumour; cancer.	
XX		
XX	Homo sapiens.	
PN	WO200224688-A2.	
XX		
PD	28-MAR-2002.	
XX		
PF	29-AUG-2001; 2001WO-US027059.	
XX		
PR	01-SEP-2000; 2000US-0236866P.	
PR	05-SEP-2000; 2000US-0230621P.	
PR	22-SEP-2000; 2000US-0235147P.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	12-JAN-2001; 2001US-0261878P.	
PR	16-JAN-2001; 2001US-0261910P.	
PR	16-JAN-2001; 2001US-0261939P.	
PR	16-JAN-2001; 2001US-0262150P.	
PR	25-JAN-2001; 2001US-0264395P.	
PR	02-FEB-2001; 2001US-0264421P.	
PR	09-FEB-2001; 2001US-0267623P.	
PR	28-FEB-2001; 2001WO-US006520.	
PR	09-MAR-2001; 2001US-0274399P.	
PR	03-APR-2001; 2001US-0280982P.	
PR	04-APR-2001; 2001US-0282129P.	
PR	04-APR-2001; 2001US-0282199P.	
PR	09-MAY-2001; 2001US-0290589P.	

KM chromosome mapping; tissue typing; pharmacogenomic; SNP; relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;

KM	single nucleotide polymorphism.
XX	
OS	Homo sapiens.
EN	WO200268649-A2.
XX	
PD	06-SEP-2002.
XX	
PF	31-JAN-2002; 2002WO-US002785.
XX	
PR	31-JAN-2001; 2001US-0265395P.
PR	31-JAN-2001; 2001US-0265412P.
PR	31-JAN-2001; 2001US-0265514P.
PR	02-FEB-2001; 2001US-0266406P.
PR	02-FEB-2001; 2001US-0266767P.
PR	07-FEB-2001; 2001US-0266975P.
PR	07-FEB-2001; 2001US-0267057P.
PR	08-FEB-2001; 2001US-0267459P.
PR	09-FEB-2001; 2001US-0267823P.
PR	15-FEB-2001; 2001US-0268974P.
PR	26-FEB-2001; 2001US-0271664P.
PR	27-FEB-2001; 2001US-0271839P.
PR	27-FEB-2001; 2001US-0271855P.
PR	02-MAR-2001; 2001US-0272788P.
PR	02-MAR-2001; 2001US-0273046P.
PR	14-MAR-2001; 2001US-0275925P.
PR	14-MAR-2001; 2001US-0275947P.
PR	14-MAR-2001; 2001US-0275950P.
PR	14-MAR-2001; 2001US-0275889P.
PR	15-MAR-2001; 2001US-0276448P.
PR	15-MAR-2001; 2001US-0276450P.
PR	16-MAR-2001; 2001US-0276639P.
PR	16-MAR-2001; 2001US-0276768P.
PR	20-MAR-2001; 2001US-0278652P.
PR	26-MAR-2001; 2001US-0278775P.
PR	26-MAR-2001; 2001US-0278787P.
PR	29-MAR-2001; 2001US-0279682P.
PR	29-MAR-2001; 2001US-0279684P.
PR	30-MAR-2001; 2001US-0280147P.
PR	11-APR-2001; 2001US-0282992P.
PR	11-APR-2001; 2001US-0283083P.
PR	20-APR-2001; 2001US-0285133P.
PR	23-APR-2001; 2001US-0285749P.
PR	03-MAY-2001; 2001US-0288327P.
PR	03-MAY-2001; 2001US-0288504P.
PR	29-MAY-2001; 2001US-0294047P.
PR	30-MAY-2001; 2001US-0294473P.
PR	08-JUN-2001; 2001US-0296646P.
PR	18-JUN-2001; 2001US-0298595P.
PR	19-JUN-2001; 2001US-0299324P.
PR	13-AUG-2001; 2001US-0312020P.
PR	16-AUG-2001; 2001US-0312689P.
PR	16-AUG-2001; 2001US-0312908P.
PR	21-AUG-2001; 2001US-0313390P.
PR	28-AUG-2001; 2001US-0315470P.
PR	31-AUG-2001; 2001US-0316447P.
PR	07-SEP-2001; 2001US-0318115P.
PR	07-SEP-2001; 2001US-0318118P.
PR	12-SEP-2001; 2001US-0318740P.
PR	19-SEP-2001; 2001US-0323379P.
PR	18-OCT-2001; 2001US-0330245P.
PR	18-OCT-2001; 2001US-0330308P.
PR	14-NOV-2001; 2001US-0332701P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
P1	Tchernev VT, Spytek KA, Zernhusen BD, Patuturajan M, Shimkets RA;
P1	Li L, Ganggoli EA, Padigan M, Anderson DW, Rastelli L, Miller CE;
P1	Griegel VJ, Tappin RJ, Guev WY, Colman SD, Wolenc AR, Pena CEA;
P1	Furtak K, Grose WM, Alsbrook UP, Lepley DW, Rieger DK, Burgess CE;
DR	WPI; 2002-706998/76.

XX N-PSDB; ADI16603.
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, typing or
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue or
 PT pharmacogenomics.
 XX
 XX
 PS Claim 1, SEQ ID NO 140; 149BP; English.
 XX
 CC This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acid.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiaesthetic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the
 CC invention.
 CC
 XX
 XX Sequence 781 AA:
 QY
 Query Match 100.0%; Score 243; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1,1e-33;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 DVASVRVAVODAPPEPAFTQAAVHLTPENKAPFTLVGQISAADLDP 48
 357 DVASVRVAVODAPPEPAFTQAAVHLTPENKAPFTLVGQISAADLDP 404
 RESULT 11
 ADI16606
 ID ADI16606 standard; protein; 781 AA.
 XX
 AC ADI16606;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human NOVX protein to treat human pathological conditions Seqid142.
 KM human, NOVX, cardiomyopathy; atherosclerosis; cancer; diabetes;
 KM inflammation; autoimmune disorder; allergy; blood disorder;
 KM acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KM immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KM Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KM cyostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
 KM haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
 KM antiaesthetic; nephrotropic; antiarthritic; hepatotropic;
 KM anasthmatic; neurotropic; antibacterial; virucide; antiparasitic;
 KM neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KM relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KM chromosome mapping; tissue typing; pharmacogenomic.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200268649-A2.

PD 06-SEP-2002.

XX 31-JAN-2002; 2002W0-US002785.

XX 31-JAN-2001; 2001US-0265395P.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 31-JAN-2001; 2001US-0265517P.

XX 02-FEB-2001; 2001US-0266406P.

XX 05-FEB-2001; 2001US-0266767P.

XX 07-FEB-2001; 2001US-0266975P.

XX 08-FEB-2001; 2001US-0267057P.

XX 09-FEB-2001; 2001US-0267459P.

XX 15-FEB-2001; 2001US-0268974P.

XX 26-FEB-2001; 2001US-0271664P.

XX 27-FEB-2001; 2001US-0271839P.

XX 02-MAR-2001; 2001US-0273788P.

XX 02-MAR-2001; 2001US-0273046P.

XX 14-MAR-2001; 2001US-0275925P.

XX 14-MAR-2001; 2001US-0275947P.

XX 14-MAR-2001; 2001US-0275950P.

XX 14-MAR-2001; 2001US-0275989P.

XX 15-MAR-2001; 2001US-0276448P.

XX 15-MAR-2001; 2001US-0276450P.

XX 16-MAR-2001; 2001US-0276397P.

XX 16-MAR-2001; 2001US-0276768P.

XX 20-MAR-2001; 2001US-0278652P.

XX 26-MAR-2001; 2001US-0278775P.

XX 26-MAR-2001; 2001US-0278778P.

XX 29-MAR-2001; 2001US-0279882P.

XX 30-MAR-2001; 2001US-0279884P.

XX 30-MAR-2001; 2001US-0280147P.

XX 11-APR-2001; 2001US-0282992P.

XX 11-APR-2001; 2001US-0283083P.

XX 20-APR-2001; 2001US-0285133P.

XX 23-APR-2001; 2001US-0285749P.

XX 03-MAY-2001; 2001US-0288327P.

XX 03-MAY-2001; 2001US-0288504P.

XX 29-MAY-2001; 2001US-0294047P.

XX 30-MAY-2001; 2001US-0294473P.

XX 08-JUN-2001; 2001US-0296644P.

XX 18-JUN-2001; 2001US-0298959P.

XX 19-JUN-2001; 2001US-0299324P.

XX 13-AUG-2001; 2001US-0312020P.

XX 16-AUG-2001; 2001US-0312889P.

XX 16-AUG-2001; 2001US-0312908P.

XX 21-AUG-2001; 2001US-0313390P.

XX 28-AUG-2001; 2001US-0315470P.

XX 31-AUG-2001; 2001US-0315447P.

XX 07-SEP-2001; 2001US-0318115P.

XX 07-SEP-2001; 2001US-0318118P.

XX 12-SEP-2001; 2001US-0318740P.

XX 19-SEP-2001; 2001US-0323379P.

XX 18-OCT-2001; 2001US-0330245P.

XX 18-OCT-2001; 2001US-0330308P.

XX 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CUPAGEN CORP.

XX Tchernev VT, Spytek KA, Zernusen BD, Patturajan M, Shinkets RA, PI Li L, Gangoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CB, PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE, PI Furek K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE, XX WPI; 2002-706998/76.

XX N-PSDB; AD116605.

XX New NOVX polypeptides and nucleic acids, useful for preventing or PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or PT pharmacogenomics.

XX Claim 1, SEQ ID NO 142; 1498bp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism.

XX Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel CC human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids.

XX The NOVX polypeptides, polynucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including CC cytoskeletal, cardiac, anti-inflammatory, immunosuppressive, anti-allergic, CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic, CC antisthmatic, nephroprotective, antirheumatic, hepatoprotective, CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic, CC relaxant and anticonvulsant. In addition, they are useful in screening CC assays to identify small molecules that modulate or inhibit, for example, CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also CC used as in chromosome mapping, tissue typing, preventive medicine and CC pharmacogenomics. This polypeptide is a human NOVX protein of the CC invention.

XX Sequence 781 AA;

XX

XX Query Match 100.0%; Score 243; DB 5; Length 781;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-23;

XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 1 DVASVRVAVQDAPBPAPFTQAAVHTVPENKAPGTLVGCISAADLDP 48

XX Db 357 DVASVRVAVQDAPBPAPFTQAAVHTVPENKAPGTLVQISAADLDP 404

XX

XX RESULT 12

XX ABR40114

XX ID ABR40114 standard; protein; 781 AA.

XX

XX ABR40114;

XX

XX 04-JUL-2003 (first entry)

XX

XX Human cell adhesion and extracellular matrix protein, CADECM-11.

XX

XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;

XX anticonvulsant; neurotropic; neuroprotective; immunosuppressive;

XX dermatological; anti-inflammatory; cytoskeletal; antiatherosclerotic;

XX Gene therapy; cell adhesion; extracellular matrix; CADECM;

XX Immune system disorder; AIDS; allergy; neurological disorder; stroke;

XX Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;

XX cerebral palsy; connective tissue disorder; systemic lupus erythematosus;

XX atherosclerosis; Alport's syndrome; cell proliferative disorder; cancer;

XX

XX Homo sapiens.

XX

XX MO2003027230-R2.

XX

XX 03-APR-2003.

XX

XX 02-AUG-2002; 2002W0-US024649.

XX

XX 03-AUG-2001; 2001US-0309964P.

XX 03-AUG-2001; 2001US-0310119P.

XX 17-AUG-2001; 2001US-0310991P.

XX 31-AUG-2001; 2001US-0316771P.

PR 07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
 PI Forsythe LJ, Elliott VS, Griffin JA, Gorvay AE, Azimzai Y;
 PI Kallack DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar U;
 XX
 DR WPI: 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1; Page 192-194; 234pp; English.
 XX
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 243; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASVRVAVQDAPPEPAFTQAAVHLTVPENKAPGTLVGQISADLDSF 48
 DB 357 DVASVRVAVQDAPPEPAFTQAAVHLTVPENKAPGTLVGQISADLDSF 404
 RESULT 13
 ADA01366
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; antiinflammatory; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 FN US2003068779-A1.
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027093.

PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI: 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 243; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASVRVAVQDAPPEPAFTQAAVHLTVPENKAPGTLVGQISADLDSF 48
 DB 357 DVASVRVAVQDAPPEPAFTQAAVHLTVPENKAPGTLVGQISADLDSF 404
 RESULT 14
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 FN US2003064474-A1.
 PD 03-APR-2003.

PF 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurley AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI; 2003-605867/57.
DR N-P-SDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 243; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DVASVRAVAVQDAPEPPAFQTAAYHLTVENKAPGTLVQGISADLDSF 48
Db 357 DVASVRAVAVQDAPEPPAFQTAAYHLTVENKAPGTLVQGISADLDSF 404
RESULT 15
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX
XX ADA43563;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DE

XX
XX Human, PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2003073196-A1.
PN
XX
XX 17-APR-2003.
PD
XX
PF 18-SEP-2002; 2002US-00245210.
XX
XX 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US027099.
XX
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurley AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI; 2003-743814/70.
DR N-P-SDB; ADA43562.
XX
PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS Claim 11; Fig 98; 307pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 243; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Dec 8 11:46:23 2004

us-09-788-051-13.rag

Page 11

CY 1 DVASVRAVQDAPEPPAFTQAAYHLLTPENKAPGTLVGOISADLDSP 48
|||
Db 357 DVASVRAVQDAPEPPAFTQAAYHLLTPENKAPGTLVGOISADLDSP 404
|||

Search completed: December 8, 2004, 10:13:06
Job time : 19.863 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243
Sequence: 1 DVASRVAVQDAPEPPAFQ.....ENKAPGTVGQISADLDSF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PTCT_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	100.0	48	10	US-09-788-051-13
2	243	100.0	193	10	US-09-788-051-15
3	243	100.0	493	15	US-10-072-012-482
4	243	100.0	607	15	US-10-258-951-74
5	243	100.0	620	10	US-09-788-051-7
6	243	100.0	636	10	US-09-788-051-4
7	243	100.0	781	9	US-09-860-868-2
8	243	100.0	781	14	US-10-245-752-98
9	243	100.0	781	14	US-10-245-859-98
10	243	100.0	781	14	US-10-245-103-98
11	243	100.0	781	14	US-10-245-107-98
12	243	100.0	781	14	US-10-245-143-98
13	243	100.0	781	14	US-10-245-771-98

14	243	100.0	781	14	US-10-245-851-98	Sequence 98, Appl
15	243	100.0	781	14	US-10-245-883-98	Sequence 98, Appl
16	243	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
17	243	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
18	243	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
19	243	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
20	243	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
21	243	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
22	243	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
23	243	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
24	243	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
25	243	100.0	781	14	US-10-239-196-98	Sequence 98, Appl
26	243	100.0	781	14	US-10-243-024-98	Sequence 98, Appl
27	243	100.0	781	14	US-10-243-409-98	Sequence 98, Appl
28	243	100.0	781	14	US-10-243-621-98	Sequence 98, Appl
29	243	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
30	243	100.0	781	14	US-10-245-033-98	Sequence 98, Appl
31	243	100.0	781	14	US-10-243-095-98	Sequence 98, Appl
32	243	100.0	781	14	US-10-243-185-98	Sequence 98, Appl
33	243	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
34	243	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
35	243	100.0	781	14	US-10-243-770-98	Sequence 98, Appl
36	243	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
37	243	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
38	243	100.0	781	14	US-10-243-320-98	Sequence 98, Appl
39	243	100.0	781	14	US-10-162-435-13	Sequence 98, Appl
40	243	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
41	243	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
42	243	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
43	243	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
44	243	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
45	243	100.0	781	14	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-13
Sequence 13, Application US/09788051
Publication No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, X. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimauc, Radolje T
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: HVS-39
CURRENT APPLICATION NUMBER: US 09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-13

Query Match 100.0%; Score 243; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DVASRVAVQDAPEPPAFQAAVHLTVENKAPGTVGQISADLDSF 48
|||||

Db 1 DVASRVAVQDAPEPPAFQAAHYHLTVPENKAPGTLVGQISAADLDSF 48

RESULT 2

US-09-788-051-15
Sequence 15, Application US/09788051
Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenhua
APPLICANT: Drmanac, Radjoe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 15
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-15

Query Match

Best Local Similarity 100.0%; Score 243; DB 10; Length 193;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 96 DVASRVAVQDAPEPPAFQAAHYHLTVPENKAPGTLVGQISAADLDSF 143

RESULT 3

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zehnusen, Bryan
APPLICANT: Patnuszjan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muraidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastrelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

Query Match

Best Local Similarity 100.0%; Score 243; DB 15; Length 493;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 357 DVASRVAVQDAPEPPAFQAAHYHLTVPENKAPGTLVGQISAADLDSF 404

RESULT 4

US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kahlack, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258,951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 243; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 6.5e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 48
Db 357 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Alterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: POLYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 243; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 6.7e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 48
Db 341 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 388

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Alterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: POLYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0

; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 243; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 6.9e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 48
Db 357 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
; FILE REFERENCE: MEMBER AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-868-2

Query Match 100.0%; Score 243; DB 9; Length 761;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 48
Db 357 DVASVRVAVQDAPEPPAFPTQAAHYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

```

; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVASRVAVQDAPEPPAFTOAAVHLTVPENKAPGTLVQISADLDSF 48
DB      357 DVASRVAVQDAPEPPAFTOAAVHLTVPENKAPGTLVQISADLDSF 404

RESULT 9
US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVASRVAVQDAPEPPAFTOAAVHLTVPENKAPGTLVQISADLDSF 48
DB      357 DVASRVAVQDAPEPPAFTOAAVHLTVPENKAPGTLVQISADLDSF 404

RESULT 10
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 357 DVASVRVAVODAPPEPAFTQAAYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 11

US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match

Best Local Similarity 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPPEPAFTQAAYHLTVPENKAPGTLVGQISADLDSP 48
Db 357 DVASVRVAVODAPPEPAFTQAAYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 12

US-10-245-143-98
; Sequence 98, Application US/10245143
; Publication No. US2003006878A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPPEPAFTQAAYHLTVPENKAPGTLVGQISADLDSP 48
Db 357 DVASVRVAVODAPPEPAFTQAAYHLTVPENKAPGTLVGQISADLDSP 404

RESULT 13

US-10-245-771-98
; Sequence 98, Application US/10245771
; Publication No. US2003006878A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114

```
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-771-98

Query Match      100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQISADIDSP 48
Db 357 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQISADIDSP 404

RESULT 14
US-10-245-851-98
/ Sequence 98, Application US/10245851
/ Publication No. US20030068782A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gueney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ CURRENT FILING DATE: 2002-09-15
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98

Query Match      100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQISADIDSP 48
Db 357 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQISADIDSP 404

RESULT 15
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gueney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-15
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Wed Dec 8 11:46:24 2004

us-09-788-051-13.rapb

Page 7

Cy 1 DVASVRAVVOAPEPPAFTQAAYHUTVPENKAPGTLVGQISAADIDSP 48
Db 357 DVASVRAVVOAPEPPAFTQAAYHUTVPENKAPGTLVGQISAADIDSP 404

Search completed: December 8, 2004, 11:34:30
Job time : 50.0484 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 5.72373 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243
Sequence: 1 DVASRYVAVQDAPEPPAPFQ.....ENKAPGTLVQGISADLDP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478:39 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	46.1	532	1	US-08-188-228-44 Sequence 44, Appl
2	112	46.1	532	1	US-08-332-638-44 Sequence 44, Appl
3	112	46.1	793	1	US-08-188-228-54 Sequence 54, Appl
4	112	46.1	793	1	US-08-332-643-48 Sequence 54, Appl
5	112	46.1	793	1	US-08-332-638-54 Sequence 54, Appl
6	112	46.1	799	1	US-08-188-228-42 Sequence 42, Appl
7	112	46.1	799	1	US-08-332-638-42 Sequence 42, Appl
8	111	45.7	693	4	US-09-819-497-55 Sequence 55, Appl
9	111	45.7	693	4	US-08-738-349-6 Sequence 55, Appl
10	111	45.7	796	2	US-08-738-349-4 Sequence 4, Appl
11	108	44.4	796	1	US-08-188-228-58 Sequence 58, Appl
12	108	44.4	796	1	US-08-332-643-52 Sequence 52, Appl
13	108	44.4	796	1	US-08-332-638-58 Sequence 58, Appl
14	108	44.4	796	2	US-08-738-349-2 Sequence 2, Appl
15	108	44.4	796	4	US-09-654-328-2 Sequence 2, Appl
16	106	43.6	794	1	US-08-188-228-60 Sequence 60, Appl
17	106	43.6	794	1	US-08-332-643-54 Sequence 54, Appl
18	106	43.6	794	1	US-08-332-638-60 Sequence 60, Appl
19	97	39.9	653	1	US-08-188-228-46 Sequence 46, Appl
20	97	39.9	653	1	US-08-332-638-46 Sequence 46, Appl
21	96.5	39.7	615	2	US-08-738-349-12 Sequence 12, Appl
22	93.5	38.5	787	1	US-08-453-695A-110 Sequence 110, Appl
23	93.5	38.5	787	1	US-08-268-161A-110 Sequence 110, Appl
24	93.5	38.5	787	3	US-08-453-702A-110 Sequence 110, Appl
25	93.5	38.5	787	3	US-09-099-639-110 Sequence 110, Appl
26	93.5	38.5	787	5	PCT-US95-08071-110 Sequence 110, Appl
27	88.5	36.4	743	4	US-09-489-847-168 Sequence 168, App

28	88.5	36.4	1026	1	US-07-998-003A-95	Sequence 95, Appl
29	88.5	36.4	1026	1	US-08-453-274B-95	Sequence 95, Appl
30	88.5	36.4	1026	1	US-08-453-695A-95	Sequence 95, Appl
31	88.5	36.4	1026	1	US-08-268-161A-95	Sequence 95, Appl
32	88.5	36.4	1026	2	US-08-453-702A-95	Sequence 95, Appl
33	88.5	36.4	1026	3	US-09-099-639-95	Sequence 95, Appl
34	88.5	36.4	1026	5	PCT-US93-12588-95	Sequence 95, Appl
35	88.5	36.4	1026	5	PCT-US95-08071-95	Sequence 95, Appl
36	88.5	36.4	1203	1	US-07-998-003A-103	Sequence 103, App
37	88.5	36.4	1203	1	US-08-453-274B-103	Sequence 103, App
38	88.5	36.4	1203	1	US-08-453-695A-103	Sequence 103, App
39	88.5	36.4	1203	1	US-08-268-161A-103	Sequence 103, App
40	88.5	36.4	1203	2	US-08-453-702A-103	Sequence 103, App
41	88.5	36.4	1203	3	US-09-099-639-103	Sequence 103, App
42	88.5	36.4	1203	5	PCT-US93-12588-103	Sequence 103, App
43	88.5	36.4	1203	5	PCT-US95-08071-103	Sequence 103, App
44	87.5	36.0	797	1	US-08-453-695A-112	Sequence 112, App
45	87.5	36.0	797	1	US-08-268-161A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shinjaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCE: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44
Query Match 46.1%; Score 112; DB 1; Length 532;
Best Local Similarity 45.7%; Pred. No. 2e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 46.1%; Score 112; DB 1; Length 793;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVPENKAPGTLVGQISADLD 46
Db 367 DTATVXIVEDADEPVPFSSPTLLVEHNAALNSVIGVTAARDP 412

RESULT 5
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 46.1%; Score 112; DB 1; Length 793;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;

Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVPENKAPGTLVGQISADLD 46
Db 367 DTATVXIVEDADEPVPFSSPTLLVEHNAALNSVIGVTAARDP 412

RESULT 6
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 46.1%; Score 112; DB 1; Length 799;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVPENKAPGTLVGQISADLD 46
Db 374 DTATVXIVEDADEPVPFSSPTLLVEHNAALNSVIGVTAARDP 419

RESULT 7
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 125
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 46.1%; Score 112; DB 1; Length 799;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPEPPATQAAYHILTPENKAPGTLVGQISAADL 46
DB 374 DTVTKIAYEDADEPMPFLAPSYIHEVENNAAGTVGRVAKDPDA 419

RESULT 8
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Duner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 45.7%; Score 111; DB 2; Length 693;
Best Local Similarity 46.8%; Pred. No. 4e-07;
Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPEPPATQAAYHILTPENKAPGTLVGQISAADL 47
DB 366 DTVTKIAYEDADEPMPFLAPSYIHEVENNAAGTVGRVAKDPDA 412

RESULT 9
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 45.7%; Score 111; DB 4; Length 693;
Best Local Similarity 46.8%; Pred. No. 4e-07;
Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPEPPATQAAYHILTPENKAPGTLVGQISAADL 47
DB 366 DTVTKIAYEDADEPMPFLAPSYIHEVENNAAGTVGRVAKDPDA 412

RESULT 10
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12

```

CORRESPONDENCE ADDRESS:
ADDRESS: Finegan, Henderson, Farabow, Garrett &
ADDRESSES: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match      45.7%; Score 111; DB 2; Length 796;
Best Local Similarity 46.8%; Pred. No. 4.7e-07;
Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

DB      1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVGOISADLDS 47
366 DVTWKIAYVEDADEPMPFLAPSYIHEVQENNAAGTVGRVHAKDPDA 412

RESULT 11
US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 559725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESSES: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
```

```

FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match      44.4%; Score 108; DB 1; Length 796;
Best Local Similarity 44.7%; Pred. No. 1.3e-06;
Matches 21; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

DB      1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVGOISADLDS 47
366 DVTWKIAYVEDADEPMPFLAPSYIHEVQENNAAGTVGRVHAKDPDA 412

RESULT 12
US-08-332-643-52
Sequence 52, Application US/08332643
Patent No. 563634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESSES: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 563634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52
```


Wed Dec 8 11:46:23 2004

us-09-788-051-13.ra1

Page 7

US-09-654-328-2

```

Query Match      44.4% Score 108; DB 4; Length 796;
Best Local Smilarity 44.7%; Pred No. 1,3e-06;
Matches      21; Conservative    10; Mismatches   16; Indels       0; Gaps      0;
QY      1 DVASRRVAPDAPPEPFAFTQAAYHITVENKAPGTLVGQISADIDS 47
Db      DTVTKRKSVEADEPFPMLTASYIHTEVENNAAGIVGRVAKKDDA 412

```

Search completed: December 8, 2004, 10:01:14
Job time : 5.72373 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 : Search time 1.29398 seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-14
Perfect score: 82
Sequence: 1 VGTSVIQVTADADDP 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	73	89.0	796 2	A38992
2	73	89.0	796 2	cadherin-11 precurs
3	73	89.0	796 2	cadherin-11 - mus
4	73	89.0	796 2	cadherin-11 - mus
5	71	86.6	785 2	OB-cadherin precurs
6	67	81.7	790 2	cadherin-7 - chick
7	67	81.7	790 2	cadherin-14 - huma
8	66	80.5	784 2	F-cadherin - Afric
9	65	79.3	789 2	cadherin 5 precurs
10	65	79.3	790 2	K-cadherin - rat
11	65	79.3	790 2	cadherin-6B - chic
12	59	72.0	793 2	cadherin-6 - human
13	56	68.3	712 1	cadherin 8 - human
14	56	68.3	713 2	T-cadherin precurs
15	56	68.3	717 2	cadherin 13 precurs
16	55	67.1	882 1	cadherin 2 - chl
17	53	64.6	794 2	cadherin 12 - huma
18	53	64.6	822 1	P-cadherin precurs
19	53	64.6	829 1	cadherin 3 precurs
20	52	63.4	877 1	N-cadherin precurs
21	52	63.4	906 1	cadherin 2 precurs
22	52	63.4	906 1	N-cadherin precurs
23	50	61.0	912 1	gamma-aminobutyrate
24	50	61.0	884 1	E-cadherin precurs
25	50	61.0	884 1	uvomoculin - mouse
26	50	61.0	4351 2	MEFPI protein - ra
27	49	59.8	732 1	B-cadherin precurs
28	49	59.8	732 1	R-cadherin precurs
29	49	59.8	913 1	A47543

30	49	59.8	913 1	IUCHCR	R-cadherin precurs
31	48	58.5	905 1	IUXLC1	N-cadherin 1 precurs
32	48	58.5	906 1	IUXLC2	N-cadherin 2 precurs
33	48	58.5	916 2	C38992	cadherin 4 precurs
34	47	57.3	458 2	AC1173	amino acid transpo
35	47	57.3	458 2	AD1530	amino acid transpo
36	47	57.3	770 2	B48910	desmocollin 1b pre
37	47	57.3	783 2	I50116	N-cadherin precurs
38	47	57.3	824 2	A48910	desmocollin 1a pre
39	47	57.3	840 2	I37281	Desca precurs
40	47	57.3	887 1	IUCHCL	Z-cadherin precurs
41	47	57.3	894 2	I37282	Dscib precurs
42	47	57.3	2610 2	T20968	hypothetical prote
43	47	57.3	3034 2	T14119	seven-pass transme
44	46	56.1	761 1	IUBODE	desmocollin 1a - b
45	46	56.1	809 1	IUBODD	desmocollin 2b pre

ALIGNMENTS

RESULT 1
A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MIM:600023
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:IJ4056; NID:g506403; PIDD:AA35622.1; PID:g50640
C/Genetics:
A/Genes: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
C/Map position: 16q22.1-16q22.1
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/58-159/Domain: cadherin repeat homology <CR2>
F/162-268/Domain: cadherin repeat homology <CR3>
F/271-383/Domain: cadherin repeat homology <CR4>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
Db 174 VGTSVIQVTADADDP 189

RESULT 2
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hofmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; MIM:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:g642796; PIDD:CA54674.1; PID:g666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
|||||
Db 174 VGTSVIQVTADADDP 189

RESULT 3
149556

cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49556
R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: I49556; MUID:95269887; PMID:7750650
A:Accession: I49556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <R88>
A:Cross-references: UNIPROT:P55288; GB:D11963; NID:G974190; PIDN:BAA06730.1; PID:G974190
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
|||||
Db 174 VGTSVIQVTADADDP 189

RESULT 4

OB-cadherin precursor - mouse
A:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amano, E.
J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D11253; NID:G994774; PIDN:BAA04797.1; PID:G994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:162-268/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:162-268/Domain: cadherin repeat homology <CR4>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
|||||
Db 174 VGTSVIQVTADADDP 189

RESULT 5
150180
cadherin-7 - chicken

C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A:Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A:Reference number: I50178; MUID:95509115; PMID:7540531
A:Accession: I50180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <NAK>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BAA07721.1; PID:G86800
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 86.6%; Score 71; DB 2; Length 785;
Best Local Similarity 87.5%; Pred. No. 0.00024;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
|||||
Db 168 VGTSVIQVTADADDP 183

RESULT 6

cadherin-14 - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02678
R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: G02678
A:Accession: G02678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <SHI>
A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AB02933.1; PID:G1389852
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 81.7%; Score 67; DB 2; Length 790;
Best Local Similarity 81.2%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
|||||
Db 174 VGTSVIQVTADADDP 189

RESULT 7

F-cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51638; S55391
R:Speseth, A.; Johnson, B.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: I51638; MUID:96035533; PMID:7496627
A:Accession: I51638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CAA59679.1; PID:G854634
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 81.7%; Score 67; DB 2; Length 790;
Best Local Similarity 81.2%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16

Db 173 VGTSLIQVATADADDP 188

RESULT 8

10H0C5

cadherin 5 precursor - human

N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: S49893; S24305; A43418

R/Bravario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp

submitted to the EMBL Data Library, June 1994

A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov

A/Reference number: S49893

A/Accession: S49893

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-784 <RES>

A/Cross-references: UNIPROT:P33151, EMBL:X79981, NID:G599833, PIDN:CAA56306.1, PID:G5998

R/Suzuki, S.; Sano, K.; Tanhara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: S24305

A/Molecule type: mRNA

A/Residues: 5-516, 'I', 518-784 <SUZ>

A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593

R/Lampugnani, M.G.; Resnati, M.; Ralfteri, M.; Pigott, R.; Pisacane, A.; Huenen, G.; Rucco,

J. Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-

A/Experimental source: cultured endothelial cells

A/Note: Sequence extracted from NCBI backbone (NCBIP:113040, NCBIP:113045, NCBIP:113047,

C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t

C/Genetics:

A/Gene: GDB:CDH5

A/Cross-references: GDB:134230; OMTM:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:1-3/Domain: signal sequence #status predicted <SIG>

F:26-47/Domain: propeptide #status predicted <PRO>

F:48-784/Product: cadherin 5 #status predicted <MAT>

F:48-593/Domain: extracellular #status predicted <EXT>

F:50-151/Domain: cadherin repeat homology <CR1>

F:154-258/Domain: cadherin repeat homology <CR2>

F:261-372/Domain: cadherin repeat homology <CR3>

F:375-479/Domain: cadherin repeat homology <CR4>

F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>

F:621-784/Domain: intracellular #status predicted <INT>

F:736-753/Region: serine-rich

F:61,112,157,362,442,523,535/Binding site: carbohydrate (asn) (covalent) #status predict

Query Match

Best Local Similarity

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLIQVATADADDP 16

Db 166 VGTSLIQVATADADDP 181

RESULT 9

152701

K-cadherin - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I52701

R/Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igataashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara,

Cancer Res. 54, 3034-3041, 1994

A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer

A/Reference number: I52701; MUID:94243827; PMID:8187093

A/Accession: I52701

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-789 <RES>

A/Cross-references: UNIPROT:P55280; GB:D25290; NID:G435460; PIDN:BA04975.1; PID:G43546

C/Genetics:

A/Gene: KCAD

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLIQVATADADDP 16

Db 174 VGTSLIQVATADADDP 189

RESULT 10

150178

cadherin-6B - chicken

C/Species: Gallus gallus (chicken)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I50178

R/Nakagawa, S.; Takeichi, M.

Development 121, 1321-1332, 1995

A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe

A/Reference number: I50178; MUID:95309115; PMID:7540531

A/Accession: I50178

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-790 <NAK>

A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:G867998; PIDN:BA07720.1; PID:G86799

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLIQVATADADDP 16

Db 174 VGTSLIQVATADADDP 189

RESULT 11

137016

cadherin-6 - human

C/Species: Homo sapiens (man)

C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C/Accession: I37016

R/Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirashashi, S.

Cancer Res. 55, 2206-2211, 1995

A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the

A/Reference number: I37016; MUID:95262134; PMID:7743525

A/Accession: I37016

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-790 <RES>

A/Cross-references: UNIPROT:P55285; GB:D31784; NID:G974184; PIDN:BA06562.1; PID:G97418

C/Genetics:

A/Gene: GDB:CDH6

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADHADDP 16
 |||:|||||
 Db 174 VGTFTVQVATDADDP 189

RESULT 12

D38992

C:Species: Homo sapiens (man)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: D38992

R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A:Reference number: 824305; PMID:91283540; PMID:2059658

A:Accession: D38992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <STU>

A:Cross-references: GB:L34060; NID:g506411; PIDN:AAA35628.1; PID:g506412

C:Genetics:

A:Gene: GDB:CDH8

A:Cross-references: GDB:5822911

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: calcium binding; cell adhesion; duplication

F:163-269/Domain: cadherin repeat homology <CDH>

Query Match Best Local Similarity 72.0%; Score 59; DB 2; Length 793;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADHADDP 16
 |||:|||||
 Db 175 LGTSTVMTATDADDP 190

RESULT 13

IOMSC1

T-cadherin precursor - chicken

N:Alternate names: truncated cadherin

C:Species: Gallus gallus (chicken)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: J00279; S33272

R:Ranscht, B.; Doures-Zimmermann, M.T.

Neuron 7, 381-402, 1991

A:Title: T-cadherin, a novel cadherin cell adhesion molecule in the nervous system lacks

A:Reference number: J00279; PMID:9200685; PMID:1654948

A:Accession: J00279

A:Molecule type: mRNA

A:Residues: 1-712 <RAN>

A:Cross-references: UNIPROT:P33150; GB:M81779; NID:g212708; PIDN:AAA49079.1; PID:g212709

A:Experimental source: embryonic brain

A:Note: Part of this sequence, including the amino end of the mature protein, was confir

R:Cunningham, H.B.; Yazaki, P.O.; Domingo, R.C.; Oades, K.V.; Bohlen, H.; Sabbadini, R.A

Arch. Biochem. Biophys. 303, 32-43, 1993

A:Title: The skeletal muscle transverse tubular Mg-ATPase: identity with Mg-ATPases of s

A:Reference number: S33272; PMID:93255565; PMID:849284

A:Accession: S33272

A:Molecule type: protein

A:Residues: 139-153 <CON>

C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought b

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:139-693/Domain: cadherin repeat homology <CDH>

F:141-245/Domain: cadherin repeat homology <CDH>

F:248-363/Domain: cadherin repeat homology <CDH>

F:366-477/Domain: cadherin repeat homology <CDH>

F:480-585/Domain: cadherin repeat homology <CDH>

F:586-691/Domain: cadherin repeat homology <CDH>

F:694-712/Domain: carboxyl-terminal propeptide #status predicted <CDH>

F:782,500,530,638,671/Binding site: carboxylate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form

Query Match Best Local Similarity 68.3%; Score 56; DB 1; Length 712;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTSTVIOVTADHADDP 16
 |||:|||||
 Db 261 GTTVMRTATDADDP 275

RESULT 14

B38992

C:Species: Homo sapiens (man)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: B38992; G02676

R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A:Reference number: 824305; PMID:91283540; PMID:2059658

A:Accession: B38992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-713 <STU>

A:Cross-references: UNIPROT:P55290; GB:L34058; NID:g506407; PIDN:AAA35624.1; PID:g506408

A:Submitted to the EMBL Data Library, May 1996

A:Reference number: H01582

A:Accession: G02676

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-713 <LEB>

A:Cross-references: EMBL:U59288; NID:g1381789; PIDN:AAE18911.1; PID:g1381790

C:Genetics:

A:Gene: GDB:CDH13

A:Cross-references: GDB:5822917; OMIM:601364

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:139-693/Domain: cadherin repeat homology <CDH>

F:141-245/Domain: cadherin repeat homology <CDH>

F:248-363/Domain: cadherin repeat homology <CDH>

F:366-477/Domain: cadherin repeat homology <CDH>

F:480-585/Domain: cadherin repeat homology <CDH>

F:586-691/Domain: cadherin repeat homology <CDH>

F:694-712/Domain: carboxyl-terminal propeptide #status predicted <CDH>

F:782,500,530,638,671/Binding site: carboxylate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match Best Local Similarity 68.3%; Score 56; DB 2; Length 713;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTSTVIOVTADHADDP 16
 |||:|||||
 Db 261 GTTVMRTATDADDP 275

RESULT 15

I51206

T-cadherin 2 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C:Accession: I51206

R:Sacristan, M.P.; Vestal, D.J.; Doures-Zimmermann, M.T.; Ranscht, B.

J. Neurosci. Res. 34, 664-680, 1993

A:Title: T-cadherin 2: molecular characterization, function in cell adhesion, and coexpr

Wed Dec 8 11:46:27 2004

us-09-788-051-14.rpt

Page 5

```

A:Reference number: 151206; MUID:93301947; PMID:8335665
A:Accession: 151206
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: tRNA
A:Residues: 1-717 <SAC>
A:Cross-references: UNIPROT:P33150; GB:S62757; NID:G3863632; PIND:AMB27242.1; PID:G386363
C:Superfamily: cadherin; cadherin repeat homology
F:248-363/Domain: cadherin repeat homology <CDH>

Query Match          68.3%  Score 56;  DB 2;  Length 717;
Best Local Similarity 66.7%;  Pred. No. 0.1;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2  GTSVTCQTATADADDP 16
      |||:::|| |||||
Db      261 GTTMRKRTAFDADDP 275

```

Search completed: December 8, 2004, 10:27:08
Job time : 1.29398 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.41322 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-14
Perfect score: 82
Sequence: 1 VGTSVIQVTADADDP 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	241	Q66TS8	Q66TS8 homo sapien
2	82	100.0	493	Q96LQ7	Q96LQ7 mus musculu
3	82	100.0	781	Q66FX6	Q66FX6 mus musculu
4	82	100.0	781	AAH57373	AAH57373 mus musculu
5	82	100.0	819	CADO_HUMAN	CADO_HUMAN
6	73	89.0	792	CADB_CHICK	CADB_CHICK
7	73	89.0	794	Q93264	Q93264 xenopus lae
8	73	89.0	796	CADB_HUMAN	CADB_HUMAN
9	73	89.0	796	CADB_MOUSE	CADB_MOUSE
10	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
11	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
12	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
13	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
14	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
15	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
16	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
17	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
18	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
19	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
20	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
21	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
22	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
23	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
24	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
25	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
26	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
27	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
28	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
29	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
30	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu
31	73	89.0	796	Q96CZ9	Q96CZ9 mus musculu

32	67	81.7	790	1	CADI_HUMAN	Q13634 homo sapien
33	67	81.7	790	2	Q8N522	Q8N522 homo sapien
34	67	81.7	790	2	Q91838	Q91838 xenopus lae
35	66	80.5	784	1	CAD5_HUMAN	P31151 homo sapien
36	66	80.5	784	1	CAD5_MOUSE	P55284 mus musculu
37	65	79.3	789	1	CAD6_RAT	P55280 rattus norv
38	65	79.3	789	1	CAD9_HUMAN	Q941B4 homo sapien
39	65	79.3	790	1	CAD6_CHICK	Q90762 gallus gall
40	65	79.3	790	1	CAD6_HUMAN	P55285 homo sapien
41	65	79.3	790	1	CAD6_MOUSE	P97326 mus musculu
42	63	76.8	390	2	Q96KY9	Q96KY9 homo sapien
43	63	76.8	772	1	CADI_HUMAN	Q94159 homo sapien
44	63	76.8	792	2	Q9DF50	Q94F80 xenopus lae
45	63	76.8	792	2	Q9DF51	Q94F81 xenopus lae

ALIGNMENTS

RESULT 1	Q66TS8	PRELIMINARY;	PRT;	241 AA.
ID	Q66TS8			
AC	Q66TS8			
DT	01-JUN-2003 (Tremblrel. 24, Created)			
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Full-length cDNA 5-PRIME end of clone CS00E010F19 of Placenta of Homo sapiens (human) (Fragment).			
DE	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Genoscopy;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Contains 2 cadherin domains.			
CC	EMBL: BX248750; CAD6557.1; -			
DR	HSP: P12830; 1065.			
DR	GO: GO:0016020; Cmembrane; IEA.			
DR	GO: GO:0005509; F:calcium ion binding; IEA.			
DR	GO: GO:0007156; P:homophilic cell adhesion; IEA.			
DR	InterPro: IPR002126; Cadherin.			
DR	Pfam: PF00028; Cadherin; 2.			
DR	PRINTS: PR00205; CADHERIN.			
DR	SMART: SMD0112; CA; 2			
DR	PROSITE: PS00232; CADHERIN_1; 1.			
DR	PROSITE: PS50268; CADHERIN_2; 2.			
KW	Calcium; Calcium-binding.			
FT	NON TER 241			
SEQUENCE	241 AA; 26348 MW; 4649831B55424604 CRC64;			
Query Match	100.0%;	Score 82;	DB 2;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 3.6e-05;		
Matches	16;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	VGTSVIQVTADADDP	16	
DB	165	VGTSVIQVTADADDP	180	
RESULT 2	Q96LQ7	PRELIMINARY;	PRT;	493 AA.
ID	Q96LQ7			
AC	Q96LQ7			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			

Qy	Db	Query Match	Best Local Similarity	Score	DB 2	Length	781
Matches	16	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
1	165	VGVSVIVQVTAHDADDP	16				
AAH57373		PRELIMINARY		PRT		781	AA
AAH57373							
02-MAR-2004		(TREMURel. 27, Created)					
02-MAR-2004		(TREMURel. 27, Last sequence update)					
02-MAR-2004		(TREMURel. 27, Last annotation update)					
Cadherin-like		24.					
CDH24							
Mus musculus (Mouse)							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
NCBI_Taxid=10090;							
SEQUENCE FROM N.A.							
STRAIN=C57BL/6; TISSUE=Brain;							
MEDLINE=22388257; PubMed=12477932;							
Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G., Klausner R.D., Collins F.S., Wanner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dietchenko L., Mannina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein W.J., Uesdi T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lodianno N.A., Peters G.J., Abramson R.D., Mullen S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A., Whitting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywiński M.I., Skalska J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.;							
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."							
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).							


```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC057373; AAH57373.1; -.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9635A CRC64;

Query Match 100.0%; Score 82; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 VGTSTVQVTAHADDP 16
Db 165 VGTSTVQVTAHADDP 180

RESULT 5
CADO_HUMAN STANDARD; PRT; 819 AA.
ID_CADO_HUMAN Q9VNT84;
AC Q86UP0; Q86UP1; Q9VNT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NC NCB1; TaxId=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CATEININS.
RA MEDLINE=2753805; PubMed=12734196; DOI=10.1101/gr.1293003;
RA Katagias B.J., Nieman M.T., Wheelock M.T., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
RL II cadherin.";
RL J. Biol. Chem. 278:27513-27519(2003).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Baton D., Foster J., Grimaldi L., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Sehagiri S., Simons L., Singh J., Smith V., Stilson U., Vagts A.,
RA Vandelan R., Watnabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood M.I.,
RA Gowdski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 3).
RP TISSUE=Testis;
RA Blum H., Baerensche S., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types. Cadherin-24 mediate strong
cell-cell adhesion.
-1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=Long form;
IsoId=Q86UP0-1; Sequence=Displayed;
Name=2; Synonyms=Short form;
IsoId=Q86UP0-2; Sequence=VSP_008717;
Name=3;
IsoId=Q86UP0-3; Sequence=VSP_008718; VSP_008719;

```

CC		Note=No experimental confirmation available;
CC	-1	SIMILARITY: Contains 5 cadherin domains.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-lib.ch).
CC		or send an email to license@isb-lib.ch .
CC		-----
DR	EMBL; AY260900; AAP05930.1; .	
DR	EMBL; AY260901; AAP05931.1; .	
DR	EMBL; AY358159; AAO88566.1; .	
DR	EMBL; AL137477; CAB0758.1; .	
DR	PIR; T46418; T46418.	
DR	HSSP; P03803; I17W.	
DR	Gnew; HGNC:14265; CDR24.	
DR	InterPro: IPRO00126; Cadherin.	
DR	InterPro: IPRO00233; Cadherin_C_term.	
DR	Pfam; PF00028; Cadherin_5.	
DR	Pfam; PF01049; Cadherin_C; 1.	
DR	PRINTS; PR00205; CADHERIN.	
DR	PROSITE; PS00232; CADHERIN_1; 2.	
DR	PROSITE; PS50268; CADHERIN_2; 5.	
KW	Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;	
KW	Multigene family; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	21 .. 44
FT	TRANSSEM	45 .. 641
FT	DONAIN	45 .. 641
FT	TRANSEM	642 .. 662
FT	DONAIN	663 .. 819
FT	DONAIN	46 .. 150
FT	DONAIN	151 .. 259
FT	DONAIN	260 .. 374
FT	DONAIN	375 .. 517
FT	DONAIN	517 .. 630
FT	CARBOHYD	446 .. 446
FT	CARBOHYD	548 .. 548
FT	CARBOHYD	563 .. 563
FT	VASPLIC	455 .. 492
FT		/FtId=VSP_008717.
FT	VASPLIC	1 .. 427
FT		/FtId=VSP_008718.
FT	VASPLIC	428 .. 492
FT		EGLHTHIAFLREARAHNLTLYLATELGMSNGPERGWPLL
FT		VAWSAPAAPQSRPVSGSAVGIPQ -> MNIVCTVCSHS
FT		ATLFSTCTHLAAYFMCFCLMLYASCGIHAAHPMFLRVNCVC
FT		VMRVCFGVLPs (in isoform 3).
FT		/FtId=VSP_008719.
SEQ	SEQUENCE	819 AA; 87751 MW; 9083034FI8BATEBA CRC64;
Oy	Query Match	100.0%; Score 82; DB 1; Length 819;
Oy	Best Local Similarity	100.0%; Pred. No. 0.00013;
Oy	Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	1 VGTSVIQVTADADDP 16	
Oy		
Oy	165 VGTSVIQVTADADDP 180	
RESULT 6		
CADB_CHICK	STANDARD;	PRT; 792 AA.
ID AC O9319;		
DT 16-OCT-2001 (Rel. 40, Created)		
DT 16-OCT-2001 (Rel. 40, Last sequence update)		
DT 05-JUL-2004 (Rel. 44, Last annotation update)		
DE Cadherin-11 precursor.		
DE Name=CDH11;		
OS Gallus gallus (Chicken);		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		


```

RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RL nervous tissue."
RL Cell Regul. 2:261-270(1991).
[4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Koolis P.F.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
molecules are detectable in both human cancer and normal cells."
RT Submitted (ARR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependant cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.
CC -1- SIMILARITY: Contains 5 cadherin domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; L34056; AAA35622.1; -
DR EMBL; D21254; BAA04798.1; -
DR EMBL; D21255; BAA04799.1; -
DR EMBL; AF0603370; AAD27755.1; -
DR EMBL; AF060368; AAD27755.1; JOINED.
DR EMBL; AF060370; AAD27756.1; -
DR EMBL; AF060369; AAD27756.1; JOINED.
DR PIR; A38992; A38992.
DR HSSP; P09803; 117M.
DR Genew; HGNC:1750; CDH11.
DR MIM; 600023; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
DR GO; GO:0001503; P:osseification; NAS.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF000028; Cadherin; 5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS0268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Repeat; S-signal; Transmembrane.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 53 Potential.
FT CHAIN 54 796 Cadherin-11.
FT DOMAIN 54 617 Extracellular (Potential).
FT TRANSMEM 618 640 Potential.
FT DOMAIN 641 796 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 150 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 612 Cadherin 5.
FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).

```

FT	CABOBYD	540	540	N-linked (GlcNAc...) (Potentia). VIVALPTLRROKREPLIVEEDNENITLYDEGGGED TEADITIONPDQINGFIR -> GCPSLMEPPSPREDNR LLYGFQLMPSYVKVRNFCLLVGVFLPLIVVAIESPT LTVLS (in isoform 2).
FT	VASAPLIC	632	693	/Frid=VSP 000640. Missing (in isoform 2).
FT	VARSPIC	694	796	/Frid-VSP 000641. RL -> SV (in Ref. 2).
FT	CONFLICT	271	272	M -> I (in Ref. 2).
FT	CONFLICT	275	275	E -> K (in Ref. 2).
FT	CONFLICT	340	340	S -> A (in Ref. 2).
FT	CONFLICT	373	373	Q -> K (in Ref. 2).
FT	CONFLICT	471	471	
SO	SEQUENCE	796 AA;	88049 MW;	2C67044CT8ADB32E CRC64;
Query Match Best Local Similarity 89.0%; Score 73; DB 1; Length 796; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Oy	1 VGTSVICVTAAHDADD 16 			
Dd	174 VGTSVICVTASDADDP 189			
RESULT 9				
ID	CADB_MOUSE	STANDARD;	PRT;	796 AA.
AC	P55288;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
De	Cadherin-11 precursor (Osteoblast-cadherin) (OB-Cadherin) (OSF-4).			
GN	Name=Cdh11; Synonyms=Cad-11;			
OC	Musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95269886; PubMed=7750649;			
RA	Hoffmann I.H., Balling R.;			
RT	"Cloning and expression analysis of a novel mesodermally expressed cadherin."			
RL	Dev. Biol. 169:337-346(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95269887; PubMed=7750650;			
RA	Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T., Miyazaki T., Takeichi M.;			
RT	"Cadherin-11 expressed in association with mesenchymal morphogenesis in the head, somite, and limb bud of early mouse embryos."			
RL	Dev. Biol. 169:347-358(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=C57BL/6; TISSUE=Calvaria;			
RA	MEDLINE=94216322; PubMed=816313;			
RA	Okaaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A., Amann E.;			
RT	"Molecular cloning and characterization of OB-cadherin, a new member of cadherin family expressed in osteoblasts."			
RL	J. Biol. Chem. 269:12092-12098(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Olfactory epithelium;			
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Rata S.-S., Loquellano N.A., Peters G.-J., Abramson R.D., Mullaly S.J.,			

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.,
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction." *Biol. Reprod.* 55:822-827(1996).
 RL Biot. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL, constitution
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X7557; CA54674.1; -;
 DR EMBL: D31963; BAA06730.1; -;
 DR EMBL: D21253; BAA04797.1; -;
 DR EMBL: BC046314; AA046314.1; -;
 DR PIR: A53584; A53584;
 DR PIR: I48277; I48277;
 DR PIR: I49556; I49556;
 DR HSP: P09803; I17W.
 DR MGD: MGI:99217; Cdh1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0005886; C:plasma membrane; IDA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR00233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin; 5.
 DR Pfam: PF01049; Cadherin_C; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS50268; CADHERIN_2; 5.
 DR KEGG: Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Cytoplasmic (Potential).
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.

FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 E -> D (in Ref. 1).
 FT CONFLICT 462 462 T -> L (in Ref. 2).
 FT CONFLICT 589 589 T -> N (in Ref. 2).
 FT CONFLICT 655 655 V -> M (in Ref. 1).
 FT CONFLICT 751 751 V -> Q (in Ref. 2).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA, 88112 MW, 0D584D24641D529 CXC64;
 QY 1 VGTSVIOVTADDDP 16
 Db 174 VGTSVIOVTADDDP 189
 Query Match 89.0%; Score 73; DB 1; Length 796;
 Best Local Similarity 93.8%; Pred. No. 0.0037;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 10
 ID 096C29 PRELIMINARY; PRT; 796 AA.
 AC 096C29;
 DT 01-DEC-2001 (TRMBLrel. 19, Created)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Struhsberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: BC013609; AA013609.1; -;
 DR HSP: P09803; I17W.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR00233; Cadherin_C_term.
 DR InterPro: IPR001901; SecE.

RA Fujinaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai I.,
RA Okazaki Y., Kuratama T., Inoue Y., Kita A., Hayashizaki Y.,
RT "MIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Spinal cord;
RA Daachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hizomoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Tasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK049652; BAC33860.1; -.
DR HSSP: P09803; 117W.
DR MGD: MGI:99217; Cdh1.
DR GO: GO:0005737; Cytoplasm; IDA.
DR GO: GO:0005866; Cytoplasmic membrane; IDA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; 5.
DR PRINTS: PRO0205; CADHERIN.
DR SMART: SM00112; Cn; 5.
DR PROSITE: PS00332; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 796 AA; 88126 MW; 71963374B2E1BE29 CRC64;
Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.0037;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy 1 VGTSVIQVTADADDP 16
Db 174 VGTSVIQVTADADDP 189
RESULT 12
Q7ZYV7 PRELIMINARY; PRT; 798 AA.
AC Q7ZYV7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE F-cadherin.
OS Gallus gallus (Chicken).
OC Archaeoptera; Melospiza; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
XM [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryonic motor neuron;
RA Shirabe K., Kimura Y., Fukushima M., Matsuo N., Yoshioke H.,
RA Tanaka H.,
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 3 cadherin domains.

```

DR EMBL: AF465257; AAC3355.1; -.
DR HSSP; P09803; 117W.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; Cadherin; 5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 3.
DR KEGG; K04400; Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 798 AA; 89156 MW; 8224F837937F106 CRC64;

Query Match
Best Local Similarity 87.8%; Score 72; DB 2; Length 798;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADADDP 16
Db 179 VGTSVIQVTADADDP 194

RESULT 13
08QGH3 PRELIMINARY; PRT; 798 AA.
ID 08QGH3
AC 08QGH3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mm-cadherin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Jessell T.M., Price S.R.;
RL Submitted (JSC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Contains 3 cadherin domains.
DR EMBL; AF459439; AAL93123.1; -.
DR HSSP; P09803; 117W.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; Cadherin; 5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 3.
DR KEGG; K04400; Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 798 AA; 89156 MW; 8224F837937F106 CRC64;

Query Match
Best Local Similarity 93.8%; Score 72; DB 2; Length 798;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADADDP 16
Db 179 VGTSVIQVTADADDP 194

RESULT 14
CADK_HUMAN

```

```

ID CADK_HUMAN STANDARD; PRT; 801 AA.
AC Q9HBT6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-20 precursor.
GN Name=CDH20; Synonyms=CDH7L3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453188; PubMed=10995570.
RA Koois P., Van Imschoot G., van Roy F.;
RT "Characterization of three novel human cadherin genes (CDH7, CDH19,
RT and CDH20) clustered on chromosome 18q22-q23 and with high homology to
RT chicken cadherin-7."
RL Genomics 68:283-295(2000).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in placenta, adult brain, and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF217289; AAG3739.1; -.
DR HSSP; P09803; 117X.
DR Genew; HGNC:1760; CDH20.
DR MIM; 605807; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; Cadherin; 5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR KEGG; K04400; Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 ? Potential.
FT PROPEP 59 ? Potential.
FT CHAIN 60 801 Cadherin-20.
FT DOMAIN 1 619 Extracellular (Potential).
FT TRANSXEM 620 640 Potential.
FT DOMAIN 641 801 Cytoplasmic (Potential).
FT DOMAIN 1 61 165 Cadherin 1.
FT DOMAIN 166 274 Cadherin 2.
FT DOMAIN 275 389 Cadherin 3.
FT DOMAIN 390 494 Cadherin 4.
FT DOMAIN 494 610 Cadherin 5.
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 420 420 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 542 542 N-linked (GlcNAc...) (Potential).
KW SEQUENCE 801 AA; 89104 MW; FB5DC35E1631866 CRC64;

Query Match
Best Local Similarity 87.8%; Score 72; DB 1; Length 801;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 VGTSVIOVTADADDP 16
 DB 180 VGTSVIOVTADADDP 195

RESULT 15

Q9Z0M3 PRELIMINARY; PRT; 801 AA.

Q9Z0M3: 01-MAY-1999 (TREMBlrel. 10. Created)
 Q9Z0M3: 01-MAY-1999 (TREMBlrel. 10. Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28. Last annotation update)
 DE Cadherin 7 precursor (Mus musculus adult male diencephalon cDNA, RIKEN
 DE full-length enriched library, clone:9330198E05 product:cadherin 7,
 DE full insert sequence).
 GN Name=Cdh20; Synonyms=Cdh7;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss random bred; TISSUE=Eye;
 RX MEDLINE=99365480; PubMed=10433813;
 RA Faulkner-Jones B.E., Godinho U.N.M., Reese B.E., Pasquini G.F.,
 RA Ruefli A., Tan S.-S.;
 RT "Cloning and expression of mouse Cadherin-7, a type-II cadherin
 RT isolated from the developing eye.";
 RL Mol. Cell. Neurosci. 14:1-16(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=99279253; PubMed=10349366;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";

RL Genome Res. 10:1757-1771(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Adachi T., Aizawa K., Akiyama T., Aikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuta M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kuwahara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AF007116; AAD01278.1; -;
 DR EMBL; AK034475; BAC28721.1; -;
 DR HSSP; P09803; 117X.
 DR MGD; MG1:1346069; Cdh20.
 DR GO; GO:0016020; C-membrane;
 DR GO; GO:0005509; F-calcium ion binding; IEA.
 DR GO; GO:007156; Phospholipid cell adhesion; IEA.
 DR DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF0028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KEGG; K04401; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 59 Potential.
 FT CHAIN 60 801 cadherin 7.
 SQ SEQUENCE 801 AA; 8897 MW; AECF5C7A2D6CFBC CRC64;

QY 1 VGTSVIOVTADADDP 16
 DB 180 VGTSVIOVTADADDP 195

Search completed: December 8, 2004, 10:24:40
 Job time : 6.41322 secs

Query Match 87.8%; Score 72; DB 2; Length 801;
 Best Local Similarity 93.8%; Pred. No. 0.0054;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.62102 Seconds

(without alignments)
666.886 Million cell updates/sec

Title: US-09-788-051-14

Perfect score: 82

Sequence: 1 VGTSVIQTADADDP 16

Scoring table: BLOSUM62

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	16	7	ADD29455 Human cad
2	82	100.0	48	7	ADD29449 Human cad
3	82	100.0	493	5	AD116946 Human NOV
4	82	100.0	607	5	ABBS3295 Human pol
5	82	100.0	620	7	ADD29448 Human cad
6	82	100.0	636	7	ADD29445 Human pol
7	82	100.0	781	5	ABBS3296 Human pol
8	82	100.0	781	5	AAW48736 Human cad
9	82	100.0	781	5	ABG34078 Human pro
10	82	100.0	781	5	AD116604 Human NOV
11	82	100.0	781	5	AD116606 Human NOV
12	82	100.0	781	6	ABR40114 Human cel
13	82	100.0	781	6	ADA01366 Human pro
14	82	100.0	781	6	ADA43795 Human sec
15	82	100.0	781	6	ADA43563 Human sec
16	82	100.0	781	6	ADA01238 Human PRO
17	82	100.0	781	6	ADA01122 Human sec
18	82	100.0	781	7	ADA43579 Human sec
19	82	100.0	781	7	ADA06941 Human PRO
20	82	100.0	781	7	ADA08429 Human PRO
21	82	100.0	781	7	ADB99722 Human PRO
22	82	100.0	781	7	ADB87005 Human PRO
23	82	100.0	781	7	ADB66160 Human sec
24	82	100.0	781	7	ADB99838 Human PRO
25	82	100.0	781	7	ADB99493 Human hum

26	82	100.0	781	7	ADB66044 Human sec
27	82	100.0	781	7	ADC23442 Human tra
28	82	100.0	781	7	ADC26135 Human PRO
29	82	100.0	781	7	ADE04962 Human PRO
30	82	100.0	781	7	ADE11268 Human PRO
31	82	100.0	781	7	ADB88199 Human PRO
32	82	100.0	781	7	ADD95494 Human sec
33	82	100.0	781	7	ADE06424 Human PRO
34	82	100.0	781	7	ADBS8199 Human PRO
35	82	100.0	781	7	ADBS8315 Human PRO
36	82	100.0	781	7	ADD90896 Human sec
37	82	100.0	781	7	ADP99451 Human sec
38	82	100.0	781	7	ADG06544 Human PRO
39	82	100.0	781	7	ADG05495 Human PRO
40	82	100.0	781	7	ADG82496 Human PRO
41	82	100.0	781	8	ADBS1749 Human sec
42	82	100.0	781	8	ADBS1865 Human sec
43	82	100.0	781	8	ADBS3723 Human sec
44	82	100.0	781	8	ADBS37607 Human sec
45	82	100.0	781	8	ADBS5378 Human sec

ALIGNMENTS

RESULT 1	
ADD29455	
ID	ADD29455 standard; peptide, 16 AA.
XX	
AC	ADD29455;
XX	
DT	15-JUN-2004 (first entry)
XX	
DE	Human cadherin-like protein peptide fragment Seq ID14.
XX	
KW	cadherin-like protein; transmembrane protein; cadherin domain;
KW	homotypic cell-cell adhesion; cytotactin; osteopontin; cancer;
KW	osteoporosis; Paget's disease; osteomalacia; hyperostosis;
KW	metastatic tumour; human.
XX	
OS	Homo sapiens.
XX	
PN	US200314491-A1.
XX	
PD	31-JUL-2003.
XX	
PF	16-FEB-2001; 2001US-00786051.
XX	
PR	03-FEB-2000; 2000US-00496914.
XX	
PR	27-APR-2000; 2000US-00560875.
XX	
PA	(GDB/) GODBOLE S. D.
PA	(KUC/) KUD C.
PA	(ARTE/) ARTERBURN M. C.
PA	(YEUN/) YEUNG G.
PA	(PALE/) PALENCIA S.
PA	(TANG/) TANG Y. T.
PA	(LIUC/) LIU C.
PA	(DRMA/) DRMANAC R. T.
XX	
PI	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI	Liu C, Drmanac RT;
XX	
DR	WPI; 2003-829799/77.
XX	
PT	Novel isolated human secreted cadherin-like polypeptide useful for
PT	treating diseases such as cancers, osteoporosis, Paget's disease,
PT	osteomalacia, hyperostosis, osteopetrosis.
XX	
PS	Claim 11; SEQ ID NO 14; 63pp; English.
XX	
CC	This invention relates to a novel isolated human secreted cadherin-like
CC	protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutic useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

CC XX SQ Sequence 16 AA;

Query Match 100.0%; Score 82; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 1 VGTSVIQVTADDDP 16

RESULT 2
ADD29449

ID ADD29449 standard; protein; 48 AA.

AC ADD29449;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein peptide fragment Seq ID8.

KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

PD 31-JUN-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496814.

PR 27-APR-2000; 2000US-00560875.

PA (GDB/) GODBOLE S D.

PA (KUC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LUC/) LIU C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 8; 63pp; English.

XX This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutic useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

CC XX SQ Sequence 48 AA;

Query Match 100.0%; Score 82; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 33 VGTSVIQVTADDDP 48

RESULT 3
AD116946

ID AD116946 standard; protein; 493 AA.

AC AD116946;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SeqID 482.

KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.

OS Homo sapiens.

PN WO20026649-A2.

PD 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 02-FEB-2001; 2001US-0265517P.

PR 05-FEB-2001; 2001US-0266406P.

PR 07-FEB-2001; 2001US-0266975P.

PR 07-FEB-2001; 2001US-0267057P.

PR 08-FEB-2001; 2001US-0267459P.

PR 09-FEB-2001; 2001US-0267823P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 27-FEB-2001; 2001US-0271855P.

PR 02-MAR-2001; 2001US-0272788P.

PR 02-MAR-2001; 2001US-0273046P.

PR 14-MAR-2001; 2001US-0275925P.

PR 14-MAR-2001; 2001US-0275947P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276788P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278778P.

PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282952P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313908P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318749P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CURAGEN CORP.

XX Tchernev VT, Spytek KA, Zernusen BD, Paturajan M, Shinketsa PA;
 PI Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
 PI Gerlach VM, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
 PI Furtak K, Grose WM, Alsobrook JP, Iepley DM, Rieger DK, Burgess CE;
 XX WPI; 2002-706998/76.

XX New NOXV polypeptides and nucleic acids, useful for preventing or
 PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Disclosure: SEQ ID NO 482; 1498pp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOXV proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOXV polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig) nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
 CC antiasmastic, nephrotoxic, antiarthritic, hepatotropic,
 CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
 CC of the invention.

XX Sequence 493 AA;

Query Match

100.0%; Score 82; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVYQVTAHDADDP 16
 DB 165 VGTSTVYQVTAHDADDP 180

RESULT 4

ID ABB53295 standard; protein; 607 AA.

AC ABB53295;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #35.

XX Human; nocrotropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquilliser; antiarrhythmic; cardiant; antiasmastic;
 KW antiinflammatory; antidiabetic; hepatotropic; virucide; antidiabetic;
 KW nephrotoxic; anorectic; cyostatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;
 PI Lai Y, Xie Q;

DR WPI; 2002-041392/05.

XX N-PSDB; ABA90360.

PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

XX Claim 1; Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 477, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 XX

Sequence 607 AA;

Query Match 100.0%; Score 82; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTAHDADDP 16
 |||||
 Db 165 VGTSVIQVTAHDADDP 180

RESULT 5
 ADD29448
 ID ADD29448 standard; protein; 620 AA.
 XX
 AC ADD29448;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human cadherin-like mature protein.

XX
 KW cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003144491-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 16-FEB-2001; 2001US-00788051.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 XX
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (GODB/) GODBOLE S D.
 PA (KUOC/) KUO C.
 PA (ARTE/) ARTERBURN M C.
 PA (YEUN/) YEUNG G.
 PA (PALE/) PALENCIA S.
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 PI Liu C, Drmanac RT;
 XX WPI; 2003-829799/77.
 XX
 PT Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX

Claim 11; SEQ ID NO 7; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutic useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the
 CC invention.
 XX

Sequence 620 AA;

Query Match 100.0%; Score 82; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTAHDADDP 16
 |||||
 Db 149 VGTSVIQVTAHDADDP 164

RESULT 6
 ADD29445
 ID ADD29445 standard; protein; 636 AA.
 XX
 AC ADD29445;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human cadherin-like protein amino acid sequence.

XX
 KW cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003144491-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 16-FEB-2001; 2001US-00788051.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 XX
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (GODB/) GODBOLE S D.
 PA (KUOC/) KUO C.
 PA (ARTE/) ARTERBURN M C.
 PA (YEUN/) YEUNG G.
 PA (PALE/) PALENCIA S.
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 PI Liu C, Drmanac RT;
 XX WPI; 2003-829799/77.
 DR N-PSDB; ADD29461, ADD29446.
 XX
 PT Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX

Claim 11; SEQ ID NO 4; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may

allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the human secreted cadherin-like protein of the invention.

Sequence 636 AA:

Query Match 100.0%; Score 82; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTAHDADP 16
D6 165 VGTSVIQVTAHDADP 180

RESULT 7
ID ABB53296 standard; protein; 781 AA.

AC ABB53296;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #36.

Human; nocotropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic; antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic; nephrotropic; anorectic; cytoskeletal; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; testicular cancer; male fertility; pancreatic disease.

OS Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

PA (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;

PI Lai Y, Xie Q;

PT WPI: 2002-041392/05.

DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

XX disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX Claim 1; Page 108-109; 116pp; English.

The invention relates to an isolated polypeptide comprising a 277, 480, 583, 584, 628, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

congestive heart failure, Hodgkin's disease and myocardial infarction; respiratory diseases including asthma, chronic obstructive pulmonary disease, cystic fibrosis and adult respiratory distress syndrome; liver diseases including hypercholesterolaemia, cirrhosis, viral and nonviral hepatitis, Type II diabetes mellitus, acute tubular necrosis and renal disease including renal failure, acute tubular necrosis and glomerulonephritis; skeletal muscle diseases including Rhabdomyolysis; myotonia congenita and interstitial obstruction; lymph diseases including lymphagiectasia; diseases of placenta including choriocarcinoma; diseases of testes including testicular cancer, male reproductive diseases including low testosterone and male infertility; and disease of pancreas including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence is a polypeptide of the invention

Sequence 781 AA:

Query Match 100.0%; Score 82; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTAHDADP 16
D6 165 VGTSVIQVTAHDADP 180

RESULT 8
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

Human; cadherin 57805; osteopathic; hepatotropic; antibacterial; antidiabetic; neuroprotective; antiarrhythmic; antineoplastic; dermatological; immunosuppressive; antiinflammatory; antipruritic; antidiabetic; antiallergic; antileptotic; haemostatic; antiapoptotic; antihypertensive; antidiabetic; antidiabetic; antidiabetic; anorectic; immunomodulatory; vasotropic; virucide; cytoskeletal; liver; thrombolytic; analgesic; anabolic; immune disorder; cardiovascular; viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis; osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy; thrombus; inflammation; infection; ischaemia; irritable bowel syndrome; gene therapy.

OS Homo sapiens.

PN WO200190145-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNITUM PHARM INC.

PI Curtis RAJ;

PT WPI: 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for

XX diagnosing and treating disorders e.g. obstructive jaundice, multiple

XX sclerosis, encephalomyelitis and atherosclerosis and to identify

XX modulators of therapeutic use.

Claim 9; Page 105; 119pp; English.
The invention relates to human cadherin family polypeptide designated

CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarrhythmic, antineumatic, dermatological,
 CC immunosuppressive, antineoplastic, antiparasitic, antisthmatic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertensive,
 CC hypotensive, antidiabetic, antineoplastic, antineoplastic, antineoplastic,
 CC immunomodulatory, vasorelaxant, antineoplastic, antineoplastic, antineoplastic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy, cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

CC XX Sequence 781 AA;
 SQ

Query Match 100.0%; Score 82; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVIGTADADDP 16
 |||||
 DB 165 VGTSTVIGTADADDP 180

RESULT 9
 ABG34078 standard; protein: 781 AA.

AC ABG34078;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human Pro peptide #49.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WC000224888-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US027099.
 XX
 PR 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264385P.
 PR 02-FEB-2001; 2001US-0264421P.
 PR 09-FEB-2001; 2001US-0267633P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282139P.
 PR 09-MAY-2001; 2001US-0280589P.
 PR 23-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GENT) GENENTECH INC.
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI; 2002-362426/39.
 DR N-PSDB; ABK70009.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 CC genetic analysis of individuals with genetic disorders.
 CC
 CC Claim 11, Fig 98; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention

CC XX Sequence 781 AA;
 SQ

Query Match 100.0%; Score 82; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVIGTADADDP 16
 |||||
 DB 165 VGTSTVIGTADADDP 180

RESULT 10
 AD116604 standard; protein: 781 AA.

AC AD116604;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human NOVX protein to treat human pathological conditions segid140.
 XX
 KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytostatic; cardiant; antineoplastic; immunosuppressive; antiallergic;
 KW haemostatic; anti-HIV; antidiabetic; antineoplastic; anorectic;
 KW antisthmatic; nephrotropic; antineoplastic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.
OS
XX WC200268649-A2.
XX
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002W0-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267453P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0276852P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0278882P.
PR 29-MAR-2001; 2001US-0278884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282952P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312888P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0333701P.
PA (CURA-) CURAGEN CORP.
XX
XX Tchernav VT, Stryek KA, Zernusen BD, Paturajan M, Shinkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE,
PI Gerlach VV, Taupier RU, Gusev VV, Colman SD, Wolenc AR, Pana CE,
PI Furtak K, Grose WM, Alsobrook JP, Lepley DK, Rieger DK, Burgess CE,
XX
XX MPI: 2002-706998/76.
DR N-PSDB; AD116603.

XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
XX Claim 1; SEQ ID NO 140; 1496bp; English.
XX
CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antisthmatic, nephrotoxic, antiarthritic, hepatocytic,
CC neuroprotective, nootropic, antibacterial, virocidic, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX Sequence 781 AA;
XX
XX
XX Query Match 100.0%; Score 82; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGTSVIQVTAHDADDP 16
Db 165 VGTSVIQVTAHDADDP 180
RESULT 11
AD116606
ID AD116606 standard; protein; 781 AA.
XX
AC AD116606;
XX
DT 15-APR-2004 (first entry)
XX
XX Human NOVX protein to treat human pathological conditions SegID142.
DE
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
XX haemostatic; anti-HIV; antidiabetic; antiatherosclerotic; anorectic;
XX antisthmatic; nephrotoxic; antiarthritic; hepatocytic;
XX neuroprotective; nootropic; antibacterial; virocidic; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
XX chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX
XX WC200268649-A2.
XX
XX PD 06-SEP-2002.

21-SEP-2001; 2001US-0324781P.
 05-OCT-2001; 2001US-0327606P.
 12-OCT-2001; 2001US-0328960P.
 09-NOV-2001; 2001US-0344471P.
 17-MAY-2002; 2002US-0381291P.
 (INCYTE GENOMICS INC.)
 Buford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
 Forsythe J, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
 Kallick DA, Xu Y, Honchell CD, Baughn MR, Gietzen KT, Lee S;
 Walla NK, Tang YT, Nguyen DB, Becha SD, Lee ST, Ramkumar J;
 WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1; Page 192-194; 234pp; English.
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 82; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSVIQVTADDDP 16
 DB 165 VGTSVIQVTADDDP 180
 RESULT 13
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 XX 09-MAY-2001; 2001US-0290589P.
 XX 29-AUG-2001; 2001WO-US027039.
 PR 18-JUL-2002; 2002US-00197942.

XX
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Matarabe CK, Wood WI, Zhang Z;
 PI Feng S;
 XX WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 CC
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 82; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSVIQVTADDDP 16
 DB 165 VGTSVIQVTADDDP 180
 RESULT 14
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO4009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003064474-A1.
 PD 03-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245859.

Wed Dec 8 11:46:25 2004

us-09-788-051-14.rag

Page 11

Db 165 VGTSVIQTADADDP 180

Search completed: December 8, 2004, 10:13:06
Job time : 6.62102 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 / Search time 16.3495 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-14
Perfect score: 82
Sequence: 1 VGTSVIQVTAHDADP 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	82	100.0	16 10 US-09-788-051-14	Sequence 14, Appl
2	82	100.0	48 10 US-09-788-051-8	Sequence 8, Appl
3	82	100.0	493 15 US-10-072-012-482	Sequence 482, Appl
4	82	100.0	607 15 US-10-258-951-74	Sequence 74, Appl
5	82	100.0	620 10 US-09-788-051-7	Sequence 7, Appl
6	82	100.0	636 10 US-09-788-051-4	Sequence 4, Appl
7	82	100.0	781 9 US-09-860-858-2	Sequence 2, Appl
8	82	100.0	781 9 US-10-245-752-98	Sequence 98, Appl
9	82	100.0	781 14 US-10-245-859-98	Sequence 98, Appl
10	82	100.0	781 14 US-10-245-103-98	Sequence 98, Appl
11	82	100.0	781 14 US-10-245-107-98	Sequence 98, Appl
12	82	100.0	781 14 US-10-245-143-98	Sequence 98, Appl
13	82	100.0	781 14 US-10-245-771-98	Sequence 98, Appl

14	82	100.0	781 14	US-10-245-851-98	Sequence 98, Appl
15	82	100.0	781 14	US-10-245-863-98	Sequence 98, Appl
16	82	100.0	781 14	US-10-237-535-98	Sequence 98, Appl
17	82	100.0	781 14	US-10-238-183-98	Sequence 98, Appl
18	82	100.0	781 14	US-10-238-263-98	Sequence 98, Appl
19	82	100.0	781 14	US-10-238-370-98	Sequence 98, Appl
20	82	100.0	781 14	US-10-245-055-98	Sequence 98, Appl
21	82	100.0	781 14	US-10-245-147-98	Sequence 98, Appl
22	82	100.0	781 14	US-10-245-730-98	Sequence 98, Appl
23	82	100.0	781 14	US-10-245-739-98	Sequence 98, Appl
24	82	100.0	781 14	US-10-246-210-98	Sequence 98, Appl
25	82	100.0	781 14	US-10-239-156-98	Sequence 98, Appl
26	82	100.0	781 14	US-10-243-024-98	Sequence 98, Appl
27	82	100.0	781 14	US-10-243-409-98	Sequence 98, Appl
28	82	100.0	781 14	US-10-245-621-98	Sequence 98, Appl
29	82	100.0	781 14	US-10-245-880-98	Sequence 98, Appl
30	82	100.0	781 14	US-10-245-033-98	Sequence 98, Appl
31	82	100.0	781 14	US-10-243-035-98	Sequence 98, Appl
32	82	100.0	781 14	US-10-245-185-98	Sequence 98, Appl
33	82	100.0	781 14	US-10-245-427-98	Sequence 98, Appl
34	82	100.0	781 14	US-10-245-473-98	Sequence 98, Appl
35	82	100.0	781 14	US-10-245-770-98	Sequence 98, Appl
36	82	100.0	781 14	US-10-245-877-98	Sequence 98, Appl
37	82	100.0	781 14	US-10-245-976-98	Sequence 98, Appl
38	82	100.0	781 14	US-10-243-320-98	Sequence 98, Appl
39	82	100.0	781 14	US-10-162-435-13	Sequence 13, Appl
40	82	100.0	781 14	US-10-242-743-98	Sequence 98, Appl
41	82	100.0	781 14	US-10-242-845-98	Sequence 98, Appl
42	82	100.0	781 14	US-10-237-636-98	Sequence 98, Appl
43	82	100.0	781 14	US-10-238-325-98	Sequence 98, Appl
44	82	100.0	781 14	US-10-238-346-98	Sequence 98, Appl
45	82	100.0	781 14	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-14
Sequence 14, Application US/09788051
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-14
Query Match 100.0%; Score 82; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VGTSVIQVTAHDADP 16
|||||

Db 1 VGTSVIQVTAHDADDP 16

RESULT 2

US-09-788-051-8

Sequence 8, Application US/09788051

Publication No. US2003014491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyn

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Lin, Chenghua

APPLICANT: Dimane, Radjef T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND

FILE REFERENCE: HVS-39

CURRENT APPLICATION NUMBER: US/09/788,051

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 48

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-8

Query Match 100.0%; Score 82; DB 10; Length 48;

Best Local Similarity 100.0%; Pred. No. 6.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VGTSVIQVTAHDADDP 16

|||||

Db 33 VGTSVIQVTAHDADDP 48

RESULT 3

US-10-072-012-482

Sequence 482, Application US/10072012

Publication No. US2004003493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar

APPLICANT: Spytek, Kimberly

APPLICANT: Zernhusen, Bryan

APPLICANT: Paturajan, Meera

APPLICANT: Shmukev, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padigaru, Murajidhara

APPLICANT: Anderson, David W.

APPLICANT: Rastelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Wolenc, Adam R.

APPLICANT: Pena, Carol E. A

APPLICANT: Furtak, Katarzyna

APPLICANT: Grosse, William M.

APPLICANT: Alsbrook II, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieser, Daniel K.

APPLICANT: Burgees, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

Query Match 100.0%; Score 82; DB 15; Length 493;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VGTSVIQVTAHDADDP 16

|||||

Db 165 VGTSVIQVTAHDADDP 180

RESULT 4

US-10-258-951-74

Sequence 74, Application US/10258951

Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj

APPLICANT: Murdoch, Paul R.

APPLICANT: Rizvi, Safia K.

APPLICANT: Smith, Randall F.

APPLICANT: Xiang, Zhaoying

APPLICANT: Kabnick, Karen

APPLICANT: Lai, Ying-Ta

APPLICANT: Xie, Qing

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GPS0025

CURRENT APPLICATION NUMBER: US/10/258,951

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: PCT/US01/13360

PRIOR FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: 60/199,963

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/203,336

PRIOR FILING DATE: 2000-05-11

PRIOR APPLICATION NUMBER: 60/207,087

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,546

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 74

LENGTH: 607

TYPE: PRT

ORGANISM: Homo sapiens

US-10-258-951-74

Query Match 100.0%; Score 82; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
DB 165 VGTSVIQVTADADDP 180

RESULT 5

US-09-788-051-7
Sequence 7, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 620
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 82; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
DB 149 VGTSVIQVTADADDP 164

RESULT 6

US-09-788-051-4
Sequence 4, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimanc, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0

SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 82; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
DB 165 VGTSVIQVTADADDP 180

RESULT 7

US-09-860-868-2
Sequence 2, Application US/09860868
Patent No. US20020076757A1
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-050001
CURRENT APPLICATION NUMBER: US/09/860,868
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/205,674
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 82; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
DB 165 VGTSVIQVTADADDP 180

RESULT 8

US-10-245-752-98
Sequence 98, Application US/10245752
Publication No. US20030064473A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C66
CURRENT APPLICATION NUMBER: US/10/245,752
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24

```

; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VGTSVIQTADADDP 16
        |||||
Db      165 VGTSVIQTADADDP 180

RESULT 9
US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VGTSVIQTADADDP 16
        |||||
Db      165 VGTSVIQTADADDP 180

RESULT 10
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US2003006878A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VGTSVIQTADADDP 16
        |||||
Db      165 VGTSVIQTADADDP 180
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VGTSVIQTADADDP 16
        |||||
Db      165 VGTSVIQTADADDP 180

RESULT 10
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US2003006878A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 VGTSVIQTADADDP 16
        |||||
Db      165 VGTSVIQTADADDP 180
```


Db 165 VGTSVIQVTAHDADDP 180

RESULT 11

```
US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C97
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Cy 1 VGTSVIQVTAHDADDP 16

Db 165 VGTSVIQVTAHDADDP 180

RESULT 12

```
US-10-245-143-98
; Sequence 98, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
```

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Matande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C90

CURRENT FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 100.0%; Score 82; DB 14; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VGTSVIQVTAHDADDP 16

Db 165 VGTSVIQVTAHDADDP 180

RESULT 13

```
US-10-245-771-98
; Sequence 98, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
```

```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98
```

```

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VGTSVIQVTAHADDP 16
Db      165 VGTSVIQVTAHADDP 180
```

```

RESULT 14
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245, 851
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
```

```

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98
```

```

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VGTSVIQVTAHADDP 16
Db      165 VGTSVIQVTAHADDP 180
```

```

RESULT 15
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98
```

```

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Wed Dec 8 11:46:26 2004

us-09-788-051-14.rapb

Page 7

Oy 1 VGTSVICVTAHADDP 16
| | | | | | | | | |
Db 165 VGTSVICVTAHADDP 180

Search completed: December 8, 2004, 11:34:30
Job time : 16.3495 secs

This Page Blank (uspio)

Query Match 89.0%; Score 73; DB 4; Length 109;
Best Local Similarity 93.8%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIOVTADDDP 16
Db 15 VGTSVIOVTASDADDP 30

RESULT 3

US-09-535-852-5
Sequence 5, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-852-5

Query Match 89.0%; Score 73; DB 4; Length 109;
Best Local Similarity 93.8%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIOVTADDDP 16
Db 15 VGTSVIOVTASDADDP 30

RESULT 4

US-08-738-349-12
Sequence 12, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-738-349-12

Query Match 89.0%; Score 73; DB 2; Length 615;
Best Local Similarity 93.8%; Pred. No. 5,4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIOVTADDDP 16
Db 167 VGTSVIOVTASDADDP 182

RESULT 5

US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-738-349-6

Query Match 89.0%; Score 73; DB 2; Length 693;
Best Local Similarity 93.8%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 174 VGTSVIQVTASDADDP 189

RESULT 6
US-09-919-497-55

Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 89.0%; Score 73; DB 4; Length 693;
Best Local Similarity 93.8%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 174 VGTSVIQVTASDADDP 189

RESULT 7
US-08-188-228-58

Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 89.0%; Score 73; DB 1; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 174 VGTSVIQVTASDADDP 189

RESULT 8
US-08-332-643-52

Sequence 52, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 89.0%; Score 73; DB 1; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16

Db 174 VGTSVIQTASDADDP 189

RESULT 9
US-08-332-638-58
Sequence 58, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 89.0%; Score 73; DB 1; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQTASDADDP 16
Db 174 VGTSVIQTASDADDP 189

RESULT 10
US-08-738-349-2
Sequence 2, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1223-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQTASDADDP 16
Db 174 VGTSVIQTASDADDP 189

RESULT 11
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 174 VGTSVIQVTADDDP 189

RESULT 12
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
TITLE OF INVENTION: Of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/153,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2:
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 89.0%; Score 73; DB 4; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 174 VGTSVIQVTADDDP 189

RESULT 13
US-09-187-859-11
Sequence 11, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-187-859-11

Query Match 86.6%; Score 71; DB 3; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 15 VGTSVIQVTADDDP 30

RESULT 14
US-09-839-542B-11
Sequence 11, Application US/09839542B
Patent No. 6563996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-839-542B-11

Query Match 86.6%; Score 71; DB 4; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
Db 15 VGTSVIQVTADDDP 30

RESULT 15
US-09-535-852-11
Sequence 11, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-535-852-11

Query Match 86.6%; Score 71; DB 4; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;

Wed Dec 8 11:46:25 2004

Matches	14;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
Cy	1	VGTSVIGVTATADDDP	16						
		:							
Db	15	VGTSVQVTATADDDP	30						

Search completed: December 8, 2004, 10:01:14
Job time : 1.90791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13; Search time 15.6086 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVQFSVETAGPCTLVGR.....APLDREARAHNLTVALTEL 193

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

PIR.79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	537	54.2	796 2	A38992
2	532	53.7	796 2	I49556
3	532	53.7	796 2	A53584
4	529	53.4	796 2	I48277
5	521	52.6	793 2	D38992
6	485	49.0	789 2	I52701
7	484	48.9	790 2	I37016
8	460	46.5	790 2	I50178
9	448	45.3	785 2	I50180
10	421	42.5	790 2	G02678
11	421	42.5	790 2	I51638
12	411	41.5	794 2	I59372
13	314.5	31.8	784 1	I0HUC5
14	229.5	23.2	5147 1	I0FFTM
15	218	22.0	814 2	G02878
16	215	21.7	2809 2	T30213
17	212.5	21.5	3034 2	T14119
18	210	21.2	730 1	I0MSCM
19	205	20.7	906 1	I0XLC2
20	203	20.5	712 1	I0MSTC
21	203	20.5	717 1	I51206
22	200	20.4	905 1	I0XLC1
23	200	20.2	887 1	I0HCHL
24	198.5	20.1	491 1	I0BOCP
25	198.5	20.1	713 2	B38992
26	196	19.8	4351 2	T00252
27	191	19.2	906 1	I0MSCN
28	190.5	19.3	827 1	A53954
29	189.5	19.1	889 2	T09055

30	188	19.0	906 1	I0HUCN	cadherin 2 precurs
31	186.5	18.8	826 2	B55363	desmocollin, type
32	186.5	18.8	832 2	S55396	Li-cadherin - huma
33	186.5	18.8	896 2	A55363	desmocollin, type
34	186	18.8	916 2	C38992	cadherin 4 precurs
35	185.5	18.7	701 2	T17243	hypothetical prote
36	185.5	18.7	912 1	I0HCHN	N-cadherin precurs
37	185.5	18.7	4307 2	T20721	hypothetical prote
38	184	18.6	829 1	I0HUCP	cadherin 3 precurs
39	183.5	18.5	822 1	I0MSCP	P-cadherin precurs
40	183	18.5	877 1	I0BOCN	N-cadherin precurs
41	182	18.4	913 1	A47543	R-cadherin precurs
42	181.5	18.3	896 2	I45858	desmocollin - bovi
43	178	18.0	913 1	I0HCHC	R-cadherin precurs
44	175.5	17.7	294 2	A54742	desmocollin 3 - mo
45	175.5	17.7	732 1	I0HCHB	B-cadherin precurs

ALIGNMENTS

RESULT 1
A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Jul-2004
C:Accession: A38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: A38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: UNIPROT:P55287; GB:I34056; NID:G506403; PIDN:AAA5622.1; PID:G50640
C:Gene(s):
A:Gene: GDB:CDH11; OB
A:Cross-references: GDB:512891; OMIM:600023
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:56-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:271-383/Domain: cadherin repeat homology <CR3>
F:386-488/Domain: cadherin repeat homology <CR4>

Query Match
Best Local Similarity 54.2%; Score 537; DB 2; Length 796;
Best Local Similarity 51.6%; Pred. No. 2.6e-39;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQFSVETAGPCTLVGRADPDLDGNALMAVSLIDEGSEAFSISTDLGRDGLTV 61
Db 272 LYMSVSEAAVQGEHGRVAKDPDLDGNGLVTVINVDGMSFETITDYTGQGVTL 331
QY 62 RKPLDPESQSYSFREYVATNTLIDPAYLRGPFKQVASRVAVQDAPEPPATQAAVHT 121
Db 332 KKVDDETERAVSLKVEANVAHIDPKFISNGPFKTVKISVEDADEPMFLAPSYIHE 391
QY 122 VPEKAPGTLVQGISADLSPAPRYSLPHSPERCFSIOPEEGTHTTAPLDREAR 181
Db 392 VQENMAAGTVGRVAKDPAANSPIRYSIDNHTDUDRFTINPEBGFIKTKPDRBEST 451
QY 182 AMENLTVALTEL 193
Db 452 AMENLTVALTEL 463

RESULT 2
I49556
cadherin-11 - mouse
C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I49556
 R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A>Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
 A/Reference number: 149556; MUID:95269887; PMID:7750650
 A/Accession: 149556
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; GB:D31963; NID:974190; PIDN:BA06730.1; PID:974191
 C/Superfamily: cadherin; cadherin repeat homology
 F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 7.1e-39; Indels 0; Gaps 0;
 Matches 98; Conservative 42; Mismatches 53;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAVSLDDEGSEAFSISTDLOGRDLT 60
 DB 271 SVYQMSVSEAAPGEEVGRVAKDPDIDGNGLVYINVDGDELFEITTDYETQGVVK 330
 QY 61 VRKLPDESQSRYSFRVEATNTLIDPAYLRGPKVAVSVAVQADAPPAATQAAHYL 120
 DB 331 LKKPVDFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGLVQGISAADLSPASPRYSILPHSDPERCFSIQPEEGTHTAAPDREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMENLVATLTEL 193
 DB 451 TAWNLISVFADAI 463

RESULT 3

OB-cadherin precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A53584
 R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Mann, E.
 J. Biol. Chem. 269, 12092-12098, 1994
 A>Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
 A/Reference number: A53584; MUID:94216322; PMID:8163513
 A/Accession: A53584
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-796 <OKA>
 A/Cross-references: UNIPROT:P55288; GB:D31253; NID:9934774; PIDN:BA04797.1; PID:9594775
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: transmembrane protein
 F:156-159/Domain: cadherin repeat homology <CR1>
 F:162-268/Domain: cadherin repeat homology <CR2>
 F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 7.1e-39; Indels 0; Gaps 0;
 Matches 98; Conservative 42; Mismatches 53;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAVSLDDEGSEAFSISTDLOGRDLT 60
 DB 271 SVYQMSVSEAAPGEEVGRVAKDPDIDGNGLVYINVDGDELFEITTDYETQGVVK 330
 QY 61 VRKLPDESQSRYSFRVEATNTLIDPAYLRGPKVAVSVAVQADAPPAATQAAHYL 120
 DB 331 LKKPVDFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGLVQGISAADLSPASPRYSILPHSDPERCFSIQPEEGTHTAAPDREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMENLVATLTEL 193

DB 451 TAWNLISVFADAI 463

RESULT 4

cadherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I48277
 R:Hoffmann, I.; Balling, R.
 Dev. Biol. 169, 337-346, 1995
 A>Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
 A/Reference number: 148277; MUID:95263886; PMID:7750649
 A/Accession: 148277
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:966666
 C/Superfamily: cadherin; cadherin repeat homology
 F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 53.4%; Score 529; DB 2; Length 796;
 Best Local Similarity 50.3%; Pred. No. 1.3e-38; Indels 0; Gaps 0;
 Matches 97; Conservative 43; Mismatches 53;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAVSLDDEGSEAFSISTDLOGRDLT 60
 DB 271 SVYQMSVSEAAPGEEVGRVAKDPDIDGNGLVYINVDGDELFEITTDYETQGVVK 330
 QY 61 VRKLPDESQSRYSFRVEATNTLIDPAYLRGPKVAVSVAVQADAPPAATQAAHYL 120
 DB 331 LKKPVDFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGLVQGISAADLSPASPRYSILPHSDPERCFSIQPEEGTHTAAPDREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMENLVATLTEL 193
 DB 451 TAWNLISVFADAI 463

RESULT 5

cadherin 8 - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
 C/Accession: D38992
 R:Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A>Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A/Reference number: S24305; MUID:91283540; PMID:2059658
 A/Accession: D38992
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-793 <SD>
 A/Cross-references: GB:I34060; NID:9506411; PIDN:AAA3628.1; PID:9506412
 C/Genetics:
 A/Gene: GDB:CDH8
 A/Cross-references: GDB:5822911
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication
 F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 52.6%; Score 521; DB 2; Length 793;
 Best Local Similarity 49.7%; Pred. No. 6.6e-38; Indels 0; Gaps 0;
 Matches 96; Conservative 41; Mismatches 56;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAVSLDDEGSEAFSISTDLOGRDLT 60

Db 272 SLVHFSVPEDEVLTGTAIGRVKANKDQIGENAKQSSYDIIDGDTALFEITSDAQADGIIR 331
 QY 61 VRKPLDFESQSYSPFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEITKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVESSPYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQENINADGKITLAPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTLVATLTEL 464

RESULT 6
 K-cadherin - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I52701
 R/Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994
 A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
 A/Reference number: I52701; MUID:94243827; PMID:8187093
 A/Accession: I52701
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-789 <RES>
 A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435461
 A/Genetics: KCAD
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 49.0%; Score 485; DB 2; Length 789;
 Best Local Similarity 46.1%; Pred. No. 9.7e-35;
 Matches 89; Conservative 44; Mismatches 60; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGTLVGRRAQDPDLGNALMAYSLIDGEGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFPTPESSPPGPIGRIRKASDADVGEMAEIYSITDGGHMFVITDQETQEGIIIT 330
 QY 61 VRKPLDFESQSYSPFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEITKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVESSPYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQENINADGKITLAPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTLVATLTEL 464

RESULT 7
 137016
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I37016
 R/Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S. Cancer Res. 55, 2206-2211, 1995
 A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the d
 A/Reference number: I37016; MUID:95562134; PMID:7743525
 A/Accession: I37016
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <RES>
 A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
 A/Genetics: CDB:CDH6

A/Cross-references: GDB:S822908
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 484; DB 2; Length 790;
 Best Local Similarity 45.1%; Pred. No. 1.2e-32;
 Matches 87; Conservative 47; Mismatches 59; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGTLVGRRAQDPDLGNALMAYSLIDGEGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFPTPESSPPGPIGRIRKASDADVGEMAEIYSITDGGHMFVITDQETQEGIIIT 330
 QY 61 VRKPLDFESQSYSPFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEITKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVESSPYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQENINADGKITLAPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTLVATLTEL 464

RESULT 8
 150178
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: I50178
 R/Nakagawa, S.; Takeichi, M. Development 121, 1321-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe
 A/Reference number: I50178; MUID:95309115; PMID:7540531
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <NAK>
 A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 46.5%; Score 460; DB 2; Length 790;
 Best Local Similarity 43.0%; Pred. No. 1.6e-32;
 Matches 83; Conservative 48; Mismatches 62; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGTLVGRRAQDPDLGNALMAYSLIDGEGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFAPASTPDPDSIGRIKANDADVDEMAEIEYSITGDSYDWFGITTDQTOGIIIT 330
 QY 61 VRKPLDFESQSYSPFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEITKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVESSPYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVKEDVPINSIGTVTAQDPDAKPNVKSVDHRHTDMRVFNINSNGSIFTSKTLREL 450
 QY 181 RAMHNTLVATLTEL 193
 Db 451 LHMHNTLVATLTEL 463

RESULT 9
 150180
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: I50180
 R/Nakagawa, S.; Takeichi, M. Development 121, 1331-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe

A:Reference number: 150178; MUID:95309115; PMID:7540531
A:Accession: 150180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <MAX>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 45.3%; Score 448; DB 2; Length 785;
Best Local Similarity 45.3%; Pred. No. 1.8e-31;
Matches 86; Conservative 38; Mismatches 66; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRRAQDPDLGNALMAYSLDGESEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNMEYKIVGDDIGYFKISVDKDTQEGITTIQ 326
QY 63 KPLPESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFTQAAYHLTV 122
DB KELPFEAKTSTTLTAIEANNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSLKISVV 386
QY 123 PENKAPGTLVGOISAADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARA 182
DB 387 SEAKVGTIIGTVAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITAKSLDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 10
G02678
cadherin-14 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
A:Accession: G02678
A:Reference number: H01584
A:Accession: G02678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <SHI>
A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:91389852; PIDN:AA02933.1; PID:9138
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 42.5%; Score 421; DB 2; Length 790;
Best Local Similarity 43.5%; Pred. No. 4.3e-29;
Matches 83; Conservative 39; Mismatches 69; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRRAQDPDLGNALMAYSLDGESEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNMEYKIVGDDIGYFKISVDKDTQEGITTIQ 326
QY 63 KPLPESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFTQAAYHLTV 122
DB KELPFEAKTSTTLTAIEANNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSLKISVV 386
QY 123 PENKAPGTLVGOISAADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARA 182
DB 387 SEAKVGTIIGTVAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITAKSLDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 11
151638
F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: 151638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion molecules
A:Reference number: 151638; MUID:96039533; PMID:7496627
A:Accession: 151638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA59679.1; PID:9854634
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 42.5%; Score 421; DB 2; Length 790;
Best Local Similarity 44.0%; Pred. No. 4.3e-29;
Matches 84; Conservative 37; Mismatches 70; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRRAQDPDLGNALMAYSLDGESEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNMEYKIVGDDIGYFKISVDKDTQEGITTIQ 326
QY 63 KPLPESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFTQAAYHLTV 122
DB KELPFEAKTSTTLTAIEANNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSLKISVV 386
QY 123 PENKAPGTLVGOISAADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARA 182
DB 387 SEAKVGTIIGTVAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITAKSLDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 12
159372
cadherin 12 - human
N:Alternate names: Br-cadherin
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
R:Seitz, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Giliham, T.C.; Kunkel, L.N.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A:Title: Expressed cadherin pseudogenes are localized to the critical region of the sprin
A:Reference number: 159372; MUID:9242541; PMID:7731968
A:Accession: 159372
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: mRNA
A:Residues: 1-794 <RBS>
A:Cross-references: UNIPROT:P55289; GB:L33477; NID:9793942; PIDN:AA048539.1; PID:9793942
C:Genetics:
A:Gene: GDB:CDH12
A:Cross-references: GDB:596324
A:Map position: 5P13-5P14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:57-160/Domain: cadherin repeat homology <CR1>
F:153-268/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>
F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 41.5%; Score 411; DB 2; Length 794;
Best Local Similarity 40.4%; Pred. No. 3.3e-28;
Matches 78; Conservative 51; Mismatches 64; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPCTLVGRRAQDPDLGNALMAYSLDGESEAFSISTDLQGRGLTV 60
DB 272 SLVQSVETAGPCTLVGRRAQDPDLGNALMAYSLDGESEAFSISTDLQGRGLTV 60
QY 61 VRKPLDESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFTQAAYHL 120

```

Db      332 LKKLDEFTKAYFKVDASNLHIDRPHSAGPKDPAATKISVLVDDEPVSFKPLTYM 391
      121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHTAAPLDREA 180
      392 EYEDTIVGTLIGAVTQGLDVLGSSAVRIFYIDWSSDSDSYFTIDNGEGTATNELLDRES 451
Qy      181 RANHLTVLATEL 193
      452 TAQNFESIASKV 464

```

RESULT 13

```

IUTUC5
caderin 5 precursor - human
N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: S49893; S24305; A43418
R/Breviarlo, F.; Cavada, L.; Conde, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784 <BR>
A/Cross-references: UNIPROT:P33151, EMBL:X79981, NID:G599833; PIDN:CMA56306.1; PID:G5998
R/Stutx, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 1, 518-784 <SU>
A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CMA42468.1; PID:G29593
R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Plascane, A.; Houen, G.; Ruco,
J. Cell Biol. 118, 1511-1522, 1992
A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A/Reference number: A43418; MUID:92394977; PMID:1522121
A/Accession: A43418
A/Molecule type: protein
A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
A/Experimental source: cultured endothelial cells
A/Note: sequence extracted from NCBI backbone (NCBI:P:113040, NCBI:P:113045, NCBI:P:113047,
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C/Genetics:
A/Gene: GDB:CDHS
A/Cross-references: GDB:134230; OMTM:601120
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-47/Domain: propeptide #status predicted <PRO>
F/48-784/Product: cadherin 5 #status predicted <MAT>
F/48-593/Domain: extracellular #status predicted <EXT>
F/50-151/Domain: cadherin repeat homology <CR1>
F/154-258/Domain: cadherin repeat homology <CR2>
F/261-372/Domain: cadherin repeat homology <CR3>
F/375-479/Domain: cadherin repeat homology <CR4>
F/481-587/Domain: cadherin repeat homology <CR5>
F/594-620/Domain: transmembrane #status predicted <TM>
F/621-784/Domain: intracellular #status predicted <INT>
F/736-753/Region: serine-rich
F/61,112,157,362,442,523,535/Binding site: carbohydrate (asn) (covalent) #status predict

```

```

Query Match      31.8%; Score 314.5; DB 1; Length 784;
Best Local Similarity 41.1%; Pred No. 1e-19;
Matches 79; Conservative 26; Mismatches 82; Indels 5; Gaps 4;
Qy      3 YQFSVETAGPGTLVGRAPQDPLGDNALMAVSLIDEGSFAFSISFDLQGRDGLTVR 62
      263 YTFVVEEDTRVGTGVSFLVEDPFOKNMTKYSILRGVQDAFIETNPANHEGIIKPM 322

```

```

Qy      63 KPLDESQSRYSFRVATNTLIDPAIYLRGPKVAVSRVAVQAPAPPAFTQAAHYLTV 122
      322 KPLDEYVYIQQSYFVEATDPTLDERY--SPKGNRAQVIINTVDDEPPIFQQPFYHQL 381
Qy      123 PEN-KAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHTAAPLDREA 181
      382 KENQKKP--LIGTVLAMPDPARHSIGYSIRTSKGFPRV-TKKGDIYNEKEDREYV 438
Qy      182 ANHLTVLATEL 193
      439 FWNVLTVKAKEL 450

```

RESULT 14

```

IUFRTM
cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Feb-1997
C/Accession: A41087; B41087
R/Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biesemann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A/Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadh
A/Reference number: A41087; MUID:92069752; PMID:1959133
A/Accession: A41087
A/Molecule type: mRNA
A/Residues: 143-485, 1279-5147 <MAH>
A/Cross-references: GB:M80537
A/Accession: B41087
A/Molecule type: DNA
A/Residues: 1-142; 487-1278 <MA2>
A/Cross-references: GB:M80537
A/Note: 1229-Gly and 1233-Ser were also found
C/Genetics:
A/Gene: fat
A/Cross-references: FlyBase:FBgn001075
C/Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>
F/36-4583/Domain: extracellular #status predicted <EXT>
F/51-156/Domain: cadherin repeat homology <CR1>
F/159-270/Domain: cadherin repeat homology <CR2>
F/271-382/Domain: cadherin repeat homology <CR3>
F/390-494/Domain: cadherin repeat homology <CR4>
F/497-599/Domain: cadherin repeat homology <CR5>
F/602-708/Domain: cadherin repeat homology <CR6>
F/718-822/Domain: cadherin repeat homology <CR7>
F/831-942/Domain: cadherin repeat homology <CR8>
F/948-1049/Domain: cadherin repeat homology <CR9>
F/1052-1153/Domain: cadherin repeat homology <CR10>
F/1156-1278/Domain: cadherin repeat homology <CR11>
F/1281-1384/Domain: cadherin repeat homology <CR12>
F/1387-1489/Domain: cadherin repeat homology <CR13>
F/1492-1601/Domain: cadherin repeat homology <CR14>
F/1607-1713/Domain: cadherin repeat homology <CR15>
F/1717-1823/Domain: cadherin repeat homology <CR16>
F/1826-1922/Domain: cadherin repeat homology <CR17>
F/1925-2021/Domain: cadherin repeat homology <CR18>
F/2028-2167/Domain: cadherin repeat homology <CR19>
F/2169-2278/Domain: cadherin repeat homology <CR20>
F/2281-2384/Domain: cadherin repeat homology <CR21>
F/2387-2491/Domain: cadherin repeat homology <CR22>
F/2494-2586/Domain: cadherin repeat homology <CR23>
F/2599-2703/Domain: cadherin repeat homology <CR24>
F/2707-2810/Domain: cadherin repeat homology <CR25>
F/2813-2913/Domain: cadherin repeat homology <CR26>
F/2915-3013/Domain: cadherin repeat homology <CR27>
F/3014-3124/Domain: cadherin repeat homology <CR28>
F/3127-3229/Domain: cadherin repeat homology <CR29>
F/3232-3334/Domain: cadherin repeat homology <CR30>
F/3337-3439/Domain: cadherin repeat homology <CR31>
F/3442-3545/Domain: cadherin repeat homology <CR32>

```

F:3548-3651/Domain: cadherin repeat homology <C32>
F:3654-3756/Domain: cadherin repeat homology <C33>
F:3954-4010/Domain: EGF homology <EG1>
F:4017-4048/Domain: EGF homology <EG2>
F:4056-4089/Domain: EGF homology <EG3>
F:4096-4127/Domain: EGF homology <EG4>
F:4584-4609/Domain: transmembrane #status predicted <TM>
F:4610-5147/Domain: intracellular #status predicted <INT>

Query Match 23.2%; Score 229.5; DB 1; Length 5147;
Best Local Similarity 33.5%; Pred. No. 3.7e-11;
Matches 64; Conservative 28; Mismatches 84; Indels 15; Gaps 7;

QY 3 YQFSVETAGPGTLVGRRAODPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLTVRKPLDPESQR 62
DB 3234 YQVIVPEHEPVGSTILIVGATDDDTGPNGLRYSISGNERQDSVDE---RTGGLVIG 3289
QY 63 KPLDPESQSRYSFVEATNTLIDPAYLRGPFKDVASVRAVQDAPE-PPAFTQAAYHLLT 121
DB 3290 QQLDYDLIQEYHNI---TVQDLYG---HPLSSVAMLLITLTDVNDNPPVFNHKEYHCY 3342
QY 122 VPENKAPGLVGOISADLDSPASP-IRYSILPHSDPERCFSTQPE-EGTHTAAPLDRE 179
DB 3343 IPENKPVGTFFQAHADKDSFKNAIHYAFLP-SGPDHFFIMQSNGTISSAVSFDYE 3401
QY 180 ARAMHNLTVLA 190
DB 3402 ERRIVTLQIXA 3412

RESULT 15

G02878
Cadherin-15 precursor - human
N/Alternate names: M-cadherin; myotubule cadherin
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02878
R/Shimoyama, Y
submitted to GenBank, February 1996
A/Reference number: H01775
A/Accession: G02878
A/Status: Preliminary; translated from GB/EMBL/DDbJ
A/Molecule type: mRNA
A/Residues: 1-814 <SH1>
A/Cross-references: UNIPROT:P55291; GB:D83542; NID:g1208423; PIDN:BAI2012.1; PID:g12084
C/Genetics:
A:Gene: GDB:CDH15; CDH14; CDH3
A:Cross-references: GDB:391031; OMIM:114019
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:155-260/Domain: cadherin repeat homology <CDH>

Query Match 22.0%; Score 218; DB 2; Length 814;
Best Local Similarity 34.7%; Pred. No. 3.5e-11;
Matches 66; Conservative 24; Mismatches 82; Indels 18; Gaps 7;

QY 14 GLTVGRRAQDPDL--GDNALMAYSLIDEGSEAFSISTDLQGRDGLTVRKPLDPESQR 71
DB 275 GVDVGRLEVEDRDPGSPNVAARFTLLEGDPGQFTIRDPKTNKEGLSIVKALDYSCSE 334
QY 72 SYSEFVEATNTL-IDPAYLR--RGPFKDVASVRAVQDAPEPPAFTQAAYHLLTVPENKAP 128
DB 335 HYEIKVSVQNEAPLQAAALAEARGQ---AKAVVHVQDNEPVPFQENPLRTSLAEGAP 390
QY 129 GLTVGOISADLDSPASPITYSLPHSDPERCFSTQPEEGTHT-----AAPLDREARA 182
DB 391 GLTVAVTFSARDPTEQIQ-RLSYSKDYDEPDLQVDAATGRIGTQHVLSPASPFK--QG 447
QY 183 WHNLTVLATE 192
DB 448 WYRAIVLAQD 457

Search completed: December 8, 2004, 10:27:09
Job time : 16.6086 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 77.3595 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVQFSVETAGPGLVGR.....APLDREAPAMHNTVLATEL 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	990	100.0	086T00	086T00 homo sapien
2	990	100.0	096L07	096L07 homo sapien
3	990	100.0	CAD0_HUMAN	CAD0_HUMAN
4	906	91.5	Q6PF56	Q6PF56 mus musculu
5	906	91.5	AAH57373	AAH57373 mus muscu
6	540	54.5	Q96C29	Q96C29 homo sapien
7	537	54.2	CADB_HUMAN	CADB_HUMAN
8	532	53.7	CADB_MOUSE	CADB_MOUSE
9	532	53.7	08C706	08C706 mus musculu
10	528	53.3	CAD8_HUMAN	CAD8_HUMAN
11	527	53.2	Q8C375	Q8C375 mus musculu
12	527	53.2	Q8C449	Q8C449 mus musculu
13	527	53.2	AAH57581	AAH57581 mus muscu
14	527	53.2	Q8BRK4	Q8BRK4 mus musculu
15	527	53.2	CAD8_MOUSE	CAD8_MOUSE
16	522	52.7	CAD8_RAT	CAD8_RAT
17	519	52.4	CAD8_CHICK	CAD8_CHICK
18	510.5	51.6	Q6PANA	Q6PANA
19	510.5	51.6	AAH60200	AAH60200 mus muscu
20	503	50.8	Q93264	Q93264 xenopus lae
21	492	49.7	Q90425	Q90425 brachydanio
22	485	49.0	CAD6_RAT	CAD6_RAT
23	484	48.9	CAD6_HUMAN	CAD6_HUMAN
24	481	48.6	CAD9_HUMAN	CAD9_HUMAN
25	467	47.2	CAD6_MOUSE	CAD6_MOUSE
26	463	46.8	CAD6_HUMAN	CAD6_HUMAN
27	460	46.5	CAD6_CHICK	CAD6_CHICK
28	459	46.4	Q80WS7	Q80WS7 mus musculu
29	459	46.4	Q8V168	Q8V168 mus musculu
30	459	46.4	AAH62962	AAH62962 mus muscu
31	457	46.2	CAD4_CHICK	P93999 gallus galli

32	448	45.3	551	2	Q8AMW2	Q8AMW2 gallus galli
33	448	45.3	785	1	CAD7_CHICK	Q90763 gallus galli
34	445	44.9	792	2	Q9DF50	Q9DF50 xenopus lae
35	444	44.8	801	1	CADK_HUMAN	Q9Ht6 homo sapien
36	441	44.5	792	2	Q9DF51	Q9DF51 xenopus lae
37	438	44.2	801	2	Q9Z0M3	Q9Z0M3 mus musculu
38	436	44.0	630	2	Q81Y78	Q81Y78 homo sapien
39	436	44.0	785	1	CAD7_HUMAN	Q9ul5 homo sapien
40	433	43.7	543	2	Q804X8	Q804X8 gallus galli
41	433	43.7	798	2	Q7ZYV7	Q7ZYV7 gallus galli
42	433	43.7	798	2	Q8G8H3	Q8G8H3 gallus galli
43	431	43.5	785	2	Q8BW92	Q8BW92 mus musculu
44	421	42.5	790	1	CADI_HUMAN	Q13634 homo sapien
45	421	42.5	790	2	Q91838	Q91838 xenopus lae

ALIGNMENTS

RESULT 1	ID	PRELIMINARY;	PRT;	370 AA.
Q86T00	Q86T00			
AC	Q86T00			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Full-length cDNA clone CS0DK003Y017 of Hela cells of Homo sapiens (human) (Fragmant).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hela cells;			
RA	Genoscope;			
RL	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.			
CC	-1- SIMILARITY: Contains 4 cadherin domains.			
DR	EMBL: BX248303; CAD62630.1; -			
DR	GO: GO:0016020; Cimerbrane; IEA.			
DR	GO: GO:000509; Fcalcium ion binding; IEA.			
DR	GO: GO:0007156; P:homophilic cell adhesion; IEA.			
DR	InterPro: IPR002126; Cadherin.			
DR	Pfam: PF00028; Cadherin; 3.			
DR	PRINTS: P000205; CADHERIN.			
DR	SMART: SM00112; CA; 2.			
DR	PROSITE: PS00232; CADHERIN_1; 1.			
DR	PROSITE: PS0268; CADHERIN_2; 4.			
KW	Calcium; Calcium-binding.			
FT	NON TER			
FT	1			
FT	370			
FT	370			
SO	SEQUENCE			
	370 AA; 39479 MW; 3996DAFA8A4500E0 CRC64;			
Query Match	100.0%; Score 990; DB 2; Length 370;			
Best Local Similarity	100.0%; Pred. No. 1.8e-72;			
Matches 193; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	SLVQFSVETAGPGLVGRADDPDIGNALMAYSLDGESEAFSISTDQGRDGLT	60	
DB	23	SLVQFSVETAGPGLVGRADDPDIGNALMAYSLDGESEAFSISTDQGRDGLT	82	
QY	61	VKKPLDFESQRSYSPVEATNTLIDPAYLRGPFDVAVRAVVDAPPPAFTQAAYL	120	
DB	83	VKKPLDFESQRSYSPVEATNTLIDPAYLRGPFDVAVRAVVDAPPPAFTQAAYL	142	
QY	121	TYPENAPGTLVGOISAADLSPASPIRSILPHSDPECFIOPEEGTHTAAPPADREA	180	
DB	143	TYPENAPGTLVGOISAADLSPASPIRSILPHSDPECFIOPEEGTHTAAPPADREA	202	

Qy 181 RAWENLT/LATEL 193
 Db 203 RAWENLT/LATEL 215

RESULT 2

Q96LQ7 PRELIMINARY; PRT; 493 AA.
 ID Q96LQ7
 AC Q96LQ7
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Nimomlya K., Wagatsuma M., Kanda K., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Kasuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isegai T., Sugano S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; AK057922; BAB71613.1; -.
 DR HSSP; P12830.1; 106S.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 4.
 DR Calciun; Calcium-binding.
 KM SEQUENCE 493 AA; 53618 MW; 33F10DF3AF09C1E CRC64;
 SQ
 Query Match 100.0%; Score 990; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2,5e-72;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLVPSVETAGRGTLVGRADDPDLDGNALMAVSLIDEGSEAFSISTDLQGRGLLT 60
 Db 262 SLVQFSVETAGPGLTGLRRAQDPDLDGNALMAVSLIDEGSEAFSISTDLQGRGLLT 321
 Qy 61 VRKPLDESSQSRYSFVEATNTLIDPAYLRGPFKVASVAVQDAPPEPAFTQAAYHL 120
 Db 322 VRKPLDESSQSRYSFVEATNTLIDPAYLRGPFKVASVAVQDAPPEPAFTQAAYHL 381
 Qy 121 TVPENKAPGTLVGQISADLDSPASPRISILPHSPERCFSIQPEEGTITHTAPIDREA 180
 Db 382 TVPENKAPGTLVGQISADLDSPASPRISILPHSPERCFSIQPEEGTITHTAPIDREA 441
 Qy 181 RAWENLT/LATEL 193
 Db 442 RAWENLT/LATEL 454

RESULT 3

CADO HUMAN
 ID CADO HUMAN STANDARD; PRT; 819 AA.
 AC Q96UP0; Q96UP0; Q96UP0;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-24 precursor (UNQ2834/PRO34003).

GN Name=CDH24; Synonyms=CDH11L;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
 RP CATELINS.
 RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
 RA Katafiasz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
 RT "Characterization of cadherin-24, a novel alternatively spliced type
 II cadherin."
 RL J. Biol. Chem. 278:27513-27519(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel P., Dowd P.,
 RA Bacon D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh U., Smith V., Stinson U., Yagci A.,
 RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment."
 RL Genome Res. 13:2265-2270(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Testis;
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. Cadherin-24 mediate strong
 CC cell-cell adhesion.
 CC -1 SUBUNIT: Associates with alpha-, beta- and delta-catenins.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Long form;
 CC IsoId=Q86UP0-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short form;
 CC IsoId=Q86UP0-2; Sequence=VSP_008717;
 CC Name=3;
 CC IsoId=Q86UP0-3; Sequence=VSP_008718, VSP_008719;
 CC Note=No experimental confirmation available.
 CC -1 SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AY260900; AAP20590.1; -.
 CC EMBL; AY260901; AAP20591.1; -.
 CC EMBL; AY358193; AA088566.1; -.
 CC EMBL; AL157477; CAB70758.1; -.
 CC PIR; T46418; T46418.
 CC HSSP; P09803; 117W.
 CC Genew; HGNC:14265; CDH24.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF01043; Cadherin; 5.
 CC Pfam; PF01043; Cadherin_C_1.
 CC PRINTS; PR00205; CADHERIN.
 CC PROSITE; PS00232; CADHERIN_1; 2.

RA Rha S.S., Locquellans N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hollyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Keltman M., Nadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Schermer A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg K.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC EMBL: BC057373; AAH57373.1; .
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin C; 1.
DR Trnna: P00026; cadherin

DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Clatium; Clatium_birdian; Cell adhesion; Transmembrane

SEQ	SEQUENCE	781 AA;	84104 MW;	1599406E6C9835AA	CRC64;
Query Match		91.5%;	Score 906;	DB 2;	Length 781;
Best Local Similarity		89.6%;	Pred. No. 2,9e-65;		
Matches 173;	Conservative	11;	Mismatches	9;	Indels 0; Gaps
QY	1	SLYQFSVETAGPGLVGR	LRAQDPDLGDNLMAVSI	LDGSGSEAFS	ISTDLQGRDGLLT
Db	262	SLYQFSVETAGPGLVGR	LKAPDDLDGNMLVAVSI	LDGSGSEVFS	ISTDSQGGDGLLT
QY	61	VKKPDLDFESQKRS	FRVEATNTLLIPATVLRGPF	KCDVASVRYAVODAE	PAFPFOAAVHL
Db	322	VKKPDLDFEFRRS	TFVEATNTLLIPATVLRGPF	KCDVASVRYAVODAE	PAFPFOATVHL
QY	121	TVKENVAPETVIGQ	ISAADLPSPAPRYSILPHSD	PERCSIOPEBETHTAA	PLDSEA

QY 181 RAWHULTVLA TEL 193
| | | | : | | |
+ + + + +

RESULT 5	
AAH57373	
ID AAH57373	PRELIMINARY;
AC AAH57373:	PRT; 781 AA.
DT 02-MAR-2004	(T-EMBLrel. 27, Created)
DT 02-MAR-2004	(T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004	(T-EMBLrel. 27, Last annotation update)

GN CDH24.
OS *Mus musculus* (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC057373; AAH57373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835NA CRC64;
 Query Match 91.5%; Score 906; DB 2; Length 781;
 Best Local Similarity 89.6%; Pred. No. 2, 9e-65;
 Matches 173; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 1 SLVQFSVETAGPGLTVGRRAQDPDIGNALMAYSILDEGSEAFSISTDGRDGLLT 60
 DB 262 SLVQFSVETAGPGLTVGRRAQDPDIGNALMAYSILDEGSEAFSISTDGRDGLLT 321
 QY 61 VRKPLDFESORSYFVREATNTLLIDPAYLRGPFKQVAVRVAVQAPPEPAFTAAYHL 120
 DB 322 VRKPLDFETRSSTFRREANTNTLLIDPAYLRGPFKQVAVRVAVQAPPEPAFTAAYHL 381
 QY 121 TVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
 DB 382 AVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 441
 QY 181 RAHNLTVLATEL 193
 DB 442 RAHNLTVLATEL 454
 RESULT 6
 Q96CZ9 PRELIMINARY; PRT; 796 AA.
 ID Q96CZ9
 AC Q96CZ9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL, BC013609; AAH13609.1; -
 DR HSP, P09803; 117M.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005509; P:calcium ion binding; IEA.
 DR GO, GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro, IPR002126; Cadherin.
 DR InterPro, IPR000233; Cadherin_C_term.
 DR InterPro, IPR001901; SECE.
 DR Pfam, PF00028; Cadherin_5.
 DR Pfam, PF01049; Cadherin_C_1.
 DR PRINTS, PR00205; CADHERIN.
 DR SMART, SMO0112; CA; 5.
 DR PROSITE, PS00232; CADHERIN_1; 3.
 DR PROSITE, PS0268; CADHERIN_2; 5.
 DR PROSITE, PS01067; SECE_SEQ; 6.
 DR KX Calcium, Calcium-binding, Cell adhesion, Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 84979B834F7547C CRC64;
 Query Match 54.5%; Score 540; DB 2; Length 796;
 Best Local Similarity 51.8%; Pred. No. 2e-35;
 Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;
 QY 1 SLVQFSVETAGPGLTVGRRAQDPDIGNALMAYSILDEGSEAFSISTDGRDGLLT 60
 DB 271 SLVQFSVETAGPGLTVGRRAQDPDIGNALMAYSILDEGSEAFSISTDGRDGLLT 330
 QY 61 VRKPLDFESORSYFVREATNTLLIDPAYLRGPFKQVAVRVAVQAPPEPAFTAAYHL 120
 DB 331 VRKPLDFETRSSTFRREANTNTLLIDPAYLRGPFKQVAVRVAVQAPPEPAFTAAYHL 390
 QY 121 TVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
 DB 391 TVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 450
 QY 181 RAHNLTVLATEL 193
 DB 451 RAHNLTVLATEL 463
 RESULT 7
 CADB_HUMAN STANDARD; PRT; 796 AA.
 ID CADB_HUMAN
 AC P55287; O15065; O15066; Q9UG93; Q9UG94;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSP-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amann E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [3]
 RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue";
 RL Cell Regul. 2:261-270(1991).
 RN [4]
 RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Koolis P.F.J., Hogendoorn P.C.W., Boyee J.V.M.G., Van Roy F.;
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RT molecules are detectable in both human cancer and normal cells";
 RL Submitted (ARR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL/ L34056; AAA5622.1; -;
 DR EMBL/ D21254; BA04798.1; -;
 DR EMBL/ D21255; BA04799.1; -;
 DR EMBL/ AF060370; AAD27755.1; -;
 DR EMBL/ AF060369; AAD27755.1; JOINED.
 DR EMBL/ AF060370; AAD27755.1; -;
 DR EMBL/ AF060369; AAD27756.1; JOINED.
 DR PIR/ A38992; A38992.
 DR HSSP/ P09803; 117W.
 DR Genew; HGNC:1750; CDH11.
 DR MIM; 600023; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.

DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 796
 FT DOMAIN 54 617
 FT TRANSMEM 618 640
 FT DOMAIN 641 796
 FT DOMAIN 54 159
 FT DOMAIN 160 268
 FT DOMAIN 269 383
 FT DOMAIN 384 486
 FT DOMAIN 487 612
 FT CARBOHYD 455 455
 FT CARBOHYD 540 540
 FT VARSPLIC 632 653
 FT
 FT VARSPLIC 694 796
 FT
 FT CONFLICT 271 272
 FT CONFLICT 275 275
 FT CONFLICT 340 340
 FT CONFLICT 373 373
 FT CONFLICT 471 471
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB2E CRC64;
 Query Match 54.2%; Score 537; DB 1; Length 796;
 Best Local Similarity 51.6%; Pred. No. 3.5e-35;
 Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;
 QY 2 LYQSVETAGPGTIVGRADPDLDGNALMAVSYILDGEGSEAFSISITDLOGRDLTV 61
 DB 272 LYQMSSEAAVAGEVGRKAKDPDIGNGLVTYIVDGDGSEFETIDYETGVIXL 331
 QY 62 KRPDPESQRSYFRVEATNLTIDPAYLRGPFKVASVRAVQAPPPATQAAHYHT 121
 DB 332 KRPVPEFETRAVSLKVEANVAHIDKFTSNGFQKTVYKISVEDADEPMTLABSYHE 391
 QY 122 VPENKAPGTLVGQISADLSDSPASPIRYSILPHSPERCFSIQPEGRTHTAPLDREAR 181
 DB 392 VQENNAAGTVVGRVAKDPDANSPRISIDHTDLDRFTINPDGFKITKPLDREBT 451
 QY 182 AMHNLTVLATEL 193
 DB 452 AMNLTVFAAEI 463
 RESULT 8
 CABD_MOUSE
 ID CABD_MOUSE STANDARD; PRT; 796 AA.
 AC P55288;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cdh11; Synonyms=Cad-11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hoffmann I.H., Balling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin";

RL Dev. Biol. 169:337-346(1995).
 RN (2)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 in the head, somite, and limb bud of early mouse embryos";
 RL Dev. Biol. 169:347-358(1995).
 RN (3)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8165113;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Aman E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN (4)
 RN SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
 RA Diatchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscin T.S., Toshyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.T., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RN DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 fetal, immature, and adult mice utilizing the polymerase chain
 reaction";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X77557; CAA54674.1; -.

DR EMBL; D31963; BAA06730.1; -.
 DR EMBL; D21253; BAA04797.1; -.
 DR EMBL; BC046314; AAH46314.1; -.
 DR PIR; A53584; A53584.
 DR PIR; I48277; I48277.
 DR PIR; I49556; I49556.
 DR HSSP; P09803; I17W.
 DR MGP; MG1:99217; Cdb11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005866; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 DR KX; KX000000; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 KW
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHD 540 540 E->D (in Ref. 1).
 FT CARBOHD 462 462 E->D (in Ref. 1).
 FT CONFLICT 589 589 T->L (in Ref. 2).
 FT CONFLICT 655 655 D->N (in Ref. 2).
 FT CONFLICT 751 751 V->M (in Ref. 1).
 FT CONFLICT 777 777 P->Q (in Ref. 1).
 FT CONFLICT 782 782 L->P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641DD529 CRC64;
 Query Match 53.7%; Score 532; DB 1; Length 796;
 Best Local Similarity 50.8%; Pred. No. 8, 3e-35;
 Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;
 QY 1 SLVPSVETKPGPTLTVGRRAQPPDLCNNALMAYSLTLDGSGEAFSISTDLCGRDILLT 60
 DB 271 SVYQMSVSEAAVPEEVEGRVAKDPDVGELVTVNIVDDGILEFTITDYETQDGVK 330
 QY 61 VRKPLDESORSYFVEATNTTLDPAVLRGPFKVASVAVQDAPPEPAFTQAAVHL 120
 DB 331 LKKPVDETRKAYSLKLEAANVHDPKELNGPKDVTYKISVEDADEPMLAPYIH 390
 QY 121 TVPNKAPGLTVGQISAADLSPASPIRYSILPHSPDERCFSTQPEEGTHTAPLDREA 180
 DB 391 EVQENAAAGTVGVRHAKDPDANSPIRYSIDRHTDLPFTINPEDGFIKTKPLDREZ 450
 QY 181 RAMNLTVLTLEL 193
 DB 451 TAWLNISVPAEI 463
 RESULT 9
 ID 08C706 PRELIMINARY; PRT; 796 AA.
 AC 08C706;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone:CS30015f15 product:cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=99279253; Pubmed=10349636;
 RA Carninci P.; Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20499374; Pubmed=11042159;
 RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
 RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20530913; Pubmed=11076861;
 RA Shibata K.; Itoh M.; Aizawa K.; Nagaoaka S.; Sasaki N.; Carninci P.;
 RA Kono H.; Akiyama T.; Nishi K.; Katsunari T.; Tashiro H.; Itoh M.;
 RA Yanamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Harada A.;
 RA Fujiwaka S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Matsumoto M.;
 RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.;
 RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA Adachi J.; Aizawa K.; Akimura T.; Arikawa T.; Bono H.; Carninci P.;
 RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.;
 RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.;
 RA Kato H.; Kawai T.; Kojima Y.; Kondo S.; Kono H.; Kouda M.; Koya S.;
 RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
 RA Nishi K.; Nomura K.; Numazaki R.; Ono M.; Oshino N.; Okazaki Y.;
 RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
 RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.;
 RA Tagawa A.; Takahashi F.; Takaku-Akahira S.; Takeda Y.; Tanaka T.;
 RA Tomaru A.; Toyota T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK049652; BAC33860.1; -
 DR HSSP; P09803; 117M.
 DR MGD; MGI:99217; Cdh1.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR002123; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 88126 MM; 7196337482E1BE29 CAC64;
 Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 8.9e-35;
 Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;
 QY 1 SLVPSVETAGPGTLVGRLLRAODPDLDGMLMAYSLDGESEAFSISTDLOGSDGLLT 60
 DB 271 SVYQMSVSEAAVGEVGEVGRVAKDPDIDENGVLVTNIVDGDGILFETITTYETQGVVK 330
 QY 61 VRKPLDFESQSESRFEATNTLLIDPAYLRGPFKDVASVAVQDAPEPPFTQAAVHL 120
 DB 331 LKKVPDFETKRAYSKIEAAVHIDPKFISNGPFQDTYVKSIVEDADEPMPFLAPSYIH 390
 QY 121 TYPENKAGETLVGQISADLDSPAPIRYSILPHSDPERCSIQPEEGTHTAAPLDREA 180
 DB 391 EVQENNAAGTIVGRVHADPDANSPIRYSIDRHTDLDLDFITNEDGFITTKYPLDKEE 450
 QY 181 RAMNLTVALTEL 193
 DB 451 TAMLNISVFAAEI 463
 RESULT 10
 CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=C8H8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Pubmed=10861224;
 RA Shimoyama Y.; Tsujimoto G.; Kitajima M.; Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.";
 RL Biochem. J. 349:159-167(2000).
 [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; Pubmed=7982033;
 RA Tanihara H.; Sano K.; Heimark R.L.; St John T.; Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; Pubmed=2059658;
 RA Suzuki S.; Sano K.; Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB035305; BAA87419.1; -
 CC EMBL: L34060; AAA35628.1; ALT_INT.
 CC HSSP: P09803; 117W.
 CC Genew: HGNC:1767; CDH8.
 CC MIM: 603008; -
 CC GO: GO:0007155; P:cell adhesion; TAG.
 CC InterPro: IPR002126; Cadherin.
 CC InterPro: IPR000233; Cadherin_C_term.
 CC Pfam: PF00028; Cadherin_5.
 CC Pfam: PF01048; Cadherin_C_1.
 CC PRINTS: PRO0205; CADHERIN.
 CC SMART: SM00112; CA; 5.
 CC PROSITE: PS00232; CADHERIN_1; 3.
 CC PROSITE: PS50268; CADHERIN_2; 5.
 CC Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC Transmembrane.
 KW SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 799 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 57 57 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 188 188 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 463 463 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 473 473 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 544 544 N-linked (GLCNAC...) (Potential).
 FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;
 Query Match 53.3%; Score 528; DB 1; Length 799;
 Best Local Similarity 50.3%; Pred. No. 1.9e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

RESULT 11

08C375
 ID 08C375 PRELIMINARY; PRT; 716 AA.
 AC 08C375;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone: D330046N17 product: cadherin 8, full insert
 DE sequence.
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10345636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtractions of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Komno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sudo N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Ikawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=11076861;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Kuroda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiramoto T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura Y.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akita S., Takeeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK086711; BAC39724.1; -
 DR HSSP: P15116; INCU.
 DR MGI: MGI:107134; Cdn8.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR002123; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR0205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 716 AA; 79149 MW; 58BD598f6638624A CRC64;
 SQ
 Query Match 53.2%; Score 527; DB 2; Length 716;
 Best Local Similarity 50.3%; Pred. No. 2e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;
 QY 1 SLVGSVETAGPTVIGRLRAQDPDGDNALMYSILDEGSEAFISTDLDGRDGLT 60
 DB 279 SLVHSPVEDVLTALGRVANQDQGENAQSSYDIDDDGTALFEITSDAQADQVIR 338
 QY 61 VRKLPDESPCRSPYFVEATNTLIDPAYLRGPFXDVASRVAVQDAPPEPAFTQAYHL 120
 DB 339 LRKLPDETEKSKYTLKAYEANAHIHIDPFSSKGPFKDIAKIVEDDEDFPVSPPYLL 398
 QY 121 TVPENKAPGTLVIGISADLDPSPSPRYSLPLPSDEPCGSIQPEEGTHTAAPLDREA 180
 DB 399 EVHENAALNSVIGQVTRAPDPDITSSPIRFSIDRHTDEROFINADDGKITLATPDREL 458
 QY 181 RAWEHLTVLATEL 193
 DB 459 SVWNITITITETI 471
 RESULT 12
 ID 08C449 PRELIMINARY; PRT; 716 AA.
 AC 08C449;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone:0630002D14 product:cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RL Mech. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690 (2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi U., Aizawa K., Akimura T., Aikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai U., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins J.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo K.F., Casavant T.L., Schetz T.E.,
 RA Brownstein W.J., Useth T.B., Toshyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.,

Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 DR EMBL; AK083092; BAC38758.1; -
 DR EMBL; BC057581; AAH57581.1; -
 DR HSSP; P15116; INCU.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; P:homophilic cell adhesion; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS02668; CADHERIN_2; 5.
 DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 KW Ca⁺⁺; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;

Query Match 53.2%; Score 527; DB 2; Length 716;
 Best Local Similarity 50.3%; Pred. No. 2e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPCTVGRVLAQDPDIDGNALMAYSILDSGESEAFSISTDLQGRGLLT 60
 DB 279 SLVHFSVPEVDVLTGTAIGRVKANDQDGENAQSYYDIIDGGTALFEITSDAQADGVIR 338
 QY 61 VRKPLDPSQSRYSFRYEATNTLLIDPAYLRGPFKDVASVAVODAPDPAPFTQAAYHL 120
 DB 339 LRKPLDPTKSKSYTLKVEANIHIDPFRSSRGPFKDTATYKIVEDADEPVSSTYLL 398
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
 DB 399 EVHENALNSVIGQVTARDPDTISSPIRFSIDRHTLERQFINADDKITLTAIPDLREL 458
 QY 181 RAMHNLVLTATEL 193
 DB 459 SWNHNTITIAETI 471

RESULT 13
 AAH57581 PRELIMINARY; PRT; 716 AA.
 ID AAH57581; PRELIMINARY; PRT; 716 AA.
 AC AAH57581; PRELIMINARY; PRT; 716 AA.
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Millar S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RI Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057581; AAH57581.1; -
 SQ SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;

Query Match 53.2%; Score 527; DB 2; Length 716;
 Best Local Similarity 50.3%; Pred. No. 2e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPCTVGRVLAQDPDIDGNALMAYSILDSGESEAFSISTDLQGRGLLT 60
 DB 279 SLVHFSVPEVDVLTGTAIGRVKANDQDGENAQSYYDIIDGGTALFEITSDAQADGVIR 338
 QY 61 VRKPLDPSQSRYSFRYEATNTLLIDPAYLRGPFKDVASVAVODAPDPAPFTQAAYHL 120
 DB 339 LRKPLDPTKSKSYTLKVEANIHIDPFRSSRGPFKDTATYKIVEDADEPVSSTYLL 398
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
 DB 399 EVHENALNSVIGQVTARDPDTISSPIRFSIDRHTLERQFINADDKITLTAIPDLREL 458
 QY 181 RAMHNLVLTATEL 193
 DB 459 SWNHNTITIAETI 471

RESULT 14
 Q8BRK4 PRELIMINARY; PRT; 754 AA.
 ID Q8BRK4; PRELIMINARY; PRT; 754 AA.
 AC Q8BRK4; PRELIMINARY; PRT; 754 AA.
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:A830083P13 product:cadherin 8, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RI "High-efficiency full-length cDNA cloning."
 RI Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RI "Functional annotation of a full-length mouse cDNA collection."
 RI Nature 409:665-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA The FANTOM Consortium;
 RI "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RI "Analysis of the mouse transcriptome based on functional annotation of
 RI 60,770 full-length cDNAs."
 RI Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;

RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.",
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20510913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system 384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kaech H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohatao N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sato K., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL; AK044046; BAC31751.1; -.
DR HSSP; P15116; INCU.
DR GO; GO:0016020; C:membrane, IEA.
DR GO; GO:0005509; P:calcium ion binding, IEA.
DR GO; GO:0007156; P:homophilic cell adhesion, IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR PRINTS; PF01049; Cadherin_C_1.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS0268; CADHERIN_2; 5.
DR KEGG; K04406; Cell adhesion, Transmembrane.
SQ SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;

Query Match 53.2%; Score 527; DB 2; Length 754;
Best Local Similarity 50.3%; Pred. No. 2, 1e-34;
Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

DB 459 SYNMHTIATETI 471

DB 459 SYNMHTIATETI 471

RESULT 15
ID CAD8_MOUSE STANDARD; PRT; 799 AA.
AC P97291;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-8 precursor.
GN Name=Cad8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=97174321; PubMed=9022055;
RA Korematsu K., Redies C.;
RT "Restricted expression of cadherin-8 in segmental and functional
RT subdivisions of the embryonic mouse brain.",
RL Dev. Dyn. 208:178-189 (1997).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
DR EMBL; X95600; CAA64857.1; -.
DR HSSP; P09803; IITW.
DR MGD; MGI:107434; Cdh8.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PF00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS0268; CADHERIN_2; 5.
DR KEGG; K04406; Cell adhesion; Glycoprotein; Repeat; Signal;
SQ Transmembrane.
FT SIGNAL 1 29
FT PROPEP 30 61
FT CHAIN 62 799
FT DOMAIN 62 621
FT TRANSMEM 622 642
FT DOMAIN 643 799
FT DOMAIN 62 167
FT DOMAIN 168 276
FT DOMAIN 277 391
FT DOMAIN 392 494
FT DOMAIN 495 616
FT CARBOHYD 188
FT CARBOHYD 463
FT CARBOHYD 473
FT CARBOHYD 544
SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 53.2%; Score 527; DB 1; Length 799;
Best Local Similarity 50.3%; Pred. No. 2, 3e-34;
Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAODPDLDGNALMAVSLDGESEAFSISTDLQGRDGLLT 60
Db 279 SLVHFSVPEDEVLGTAIGRVXANDQDIGENAOSSYDIIDGDTALFEITSDAQODGVIR 338
QY 61 VRKPLDEFSORSVSEFVEATNTLIDPAYLRGPEKDVASVRAVODAPPEPAFTQAAYHL 120
Db 339 LRKPLDEETKKSITLVKVEANIHIDRFSSRGPPKDTATVIVVEDADPEPVSPTYL 398
QY 121 TVPENKAPGLVQISAADLSPASPIRYSILPHSDPERCFSIQPEGTIHTAAPLDREA 180
Db 399 EVHENAALNSVIGQVTARDPDITSSPIRFSIDRHTDLERQFNINADDGKITLATPLDREL 458
QY 181 RAHNLTVLATTEL 193
Db 459 SVMHNTITIAETI 471

Search completed: December 8, 2004, 10:24:41
Job time : 78.3595 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 79.866 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVGFSTVERNAGPGLVGR.....APDRARAHNLTVALTEL 193

Scoring table: BLASTN62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	990	100.0	193	7	ADD29456 Human cad
2	990	100.0	493	5	AD116946 Human NOV
3	990	100.0	607	5	ABB53295 Human pol
4	990	100.0	620	7	ADD29448 Human cad
5	990	100.0	636	7	ADD29445 Human cad
6	990	100.0	781	5	ABB53296 Human pol
7	990	100.0	781	5	AM48736 Human cad
8	990	100.0	781	5	ABG34078 Human PRO
9	990	100.0	781	5	AD116606 Human NOV
10	990	100.0	781	6	ABR40114 Human cel
11	990	100.0	781	6	ADA01366 Human PRO
12	990	100.0	781	6	ADA43795 Human sec
13	990	100.0	781	6	ADA43563 Human sec
14	990	100.0	781	6	ADA01238 Human PRO
15	990	100.0	781	7	ADA01122 Human sec
16	990	100.0	781	7	ADA43679 Human sec
17	990	100.0	781	7	ADA06941 Human PRO
18	990	100.0	781	7	ADA08429 Human hum
19	990	100.0	781	7	ADB99722 Human PRO
20	990	100.0	781	7	ADB87005 Human PRO
21	990	100.0	781	7	ADB66160 Human sec
22	990	100.0	781	7	ADB99838 Human PRO
23	990	100.0	781	7	ADB99493 Human hum
24	990	100.0	781	7	ADB66044 Human sec
25	990	100.0	781	7	ADC23442 Human tra

ALIGNMENTS

25	990	100.0	781	7	ADC26135	Adc26135 Human PRO
26	990	100.0	781	7	AD504962	Ad504962 Human PRO
27	990	100.0	781	7	AD111268	Ad111268 Human PRO
28	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
29	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
30	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
31	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
32	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
33	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
34	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
35	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
36	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
37	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
38	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
39	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
40	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
41	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
42	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
43	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
44	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO
45	990	100.0	781	7	ADDB8199	AdDB8199 Human PRO

RESULT 1
ADD29456
ID ADD29456 standard; protein; 193 AA.

AC ADD29456;
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID15.

KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytostatic; osteopetrotic; cancer;
KW osteopetrotic; Paget's disease; osteomalacia; hyperostosis; osteopetrotosis;
KW metastatic tumour; human.

OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.

XX
PF 16-FEB-2001; 2001US-00788051.

XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.

XX
PA (GDB/) GDBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIT C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
Liu C, Drmanac RT;
XX
DR WPI; 2003-829799/77.
DR N-PSDB; ADD29456.

XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
treating diseases such as cancers, osteopetrotosis, Paget's disease,
osteomalacia, hyperostosis, osteopetrotosis.
PT
PS Claim 11; SEQ ID NO 15; 63pp; English.

XX
CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutic useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of a peptide fragment of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

SQ Sequence 193 AA;

Query Match 100.0%; Score 990; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 7, 5e-101;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETGAPPTLVGRRLAOPDLDGNALMAVSTLDEGSEAFSITDLGRRGLLT 60
Db 1 SLVQSVETGAPPTLVGRRLAOPDLDGNALMAVSTLDEGSEAFSITDLGRRGLLT 60
QY 61 VRKPLDESPQSRYSFVEAINTLLIDPAYLRGPKQVAVVAVQDAPEPPAFTQAAYH 120
Db 61 VRKPLDESPQSRYSFVEAINTLLIDPAYLRGPKQVAVVAVQDAPEPPAFTQAAYH 120
QY 121 TVEPKAPGTLVQGISADLDSPASPTRYSLPHSDPERCFSTOPEGTHHTAALPDEA 180
Db 121 TVEPKAPGTLVQGISADLDSPASPTRYSLPHSDPERCFSTOPEGTHHTAALPDEA 180
QY 181 RAWENLTVALTEL 193
Db 181 RAWENLTVALTEL 193

RESULT 2

AD116946
ID AD116946 standard; protein; 493 AA.

AC AD116946;

DT 15-APR-2004 (first entry)

DB Human NOVX protein homologue SegID 482.

KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.

OS Homo sapiens.

PN WO200268649-A2.

PD 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 02-FEB-2001; 2001US-0266466P.

PR 05-FEB-2001; 2001US-0266767P.

PR 07-FEB-2001; 2001US-0266975P.

PR 08-FEB-2001; 2001US-0267459P.

PR 09-FEB-2001; 2001US-0267833P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 29-MAR-2001; 2001US-0278882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-MAY-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312028P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

XX Tchernev VT, Spytek KA, Zernusen BD, Patturajan M, Shinkets RA;
XX Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
XX Gerlach VN, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI, 2002-706998/76.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.

PS Disclosure; SEQ ID NO 482; 1498bp; English.

XX This invention relates to a novel nucleic acids, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments for
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytoskeletal, cardiant, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiaesthetic, neurotropic, antiaerobic, hepatotropic,
 CC neuroprotective, neurotropic, antibacterial, vitucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.

XX Sequence 493 AA;

Query Match 100.0%; Score 990; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-100;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 SLVPSVETAGPTVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
 262 SLVPSVETAGPTVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
 QY VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 120
 DB VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 361
 322 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 361
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 441
 QY 181 RAMHNLTVLATEL 193
 DB 442 RAMHNLTVLATEL 454

RESULT 3
 ABB53295
 ID ABB53295 standard; protein; 607 AA.

XX ABB53295;

DT 12-FEB-2002 (first entry)

XX Human polypeptide #35.

Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiaesthetic;
 KW antiinflammatory; antidiabetic; hepatotropic; virucide; antidiabetic;
 KW nephrotoxic; anorectic; cytoskeletal; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-020336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMTK) SMITHKLINE BEECHAM CORP.

XX (SMTK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kadnick KS,
 XX Lai Y, Xie Q;
 XX WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX Claim 1, Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 359, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneoplastic disease, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, acute tubular necrosis and
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Duchenne's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 607 AA;

Query Match 100.0%; Score 990; DB 5; Length 607;

Best Local Similarity 100.0%; Pred. No. 3.9e-100;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVPSVETAGPTVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
 DB 262 SLVPSVETAGPTVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
 QY VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 120
 DB VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 361
 322 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPPAFTQAAYHL 361
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 441
 QY 181 RAMHNLTVLATEL 193
 DB 442 RAMHNLTVLATEL 454

RESULT 4
 ADD29448
 ID ADD29448 standard; protein; 620 AA.

XX ADD29448;

XX 15-JUN-2004 (first entry)

XX Human cadherin-like mature protein.

KW cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytoskeletal; osteopontin; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.

XX Homo sapiens.

XX US2003144491-A1.

```

XX 31-JUL-2003.
PD 16-FEB-2001; 2001US-00788051.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX (GODB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIT C.
PA (DRMA/) DRMANAC R T.
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
PI Liu C, Drmanac RT;
XX WPI; 2003-829799/77.
XX Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX Claim 11; SEQ ID NO 7; 63pp; English.
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of
XX transmembrane proteins which share a common cadherin domain in their
XX extracellular region. The extracellular portion mediates homotypic cell-
XX cell adhesion that is calcium dependent. Modulators of the invention of the
XX invention may have cytostatic or osteopathic activity. The invention may
XX allow development of therapeutics useful for the treatment of diseases
XX such as cancers, osteoporosis, Paget's disease, osteomalacia,
XX hyperostosis and osteopetrosis. The protein and DNA sequence of the
XX invention may also be useful as markers for prognosis of metastatic
XX tumours. The present sequence is that of the mature human secreted
XX cadherin-like protein which was used during the exemplification of the
XX invention.
SQ Sequence 620 AA;
Query Match 100.0%; Score 990; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 4e-100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPCTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 60
DB 246 SLVQFSVETAGPCTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 305
QY 61 VRKPLDESGQSYSFREATNTLIDPAYLRGPFKVAVSVAVVQDAPPEPPTQAAVHL 120
DB 306 VRKPLDESGQSYSFREATNTLIDPAYLRGPFKVAVSVAVVQDAPPEPPTQAAVHL 365
QY 121 TVPENKAPGTLVGOISADLDSPASPPIRYISILPHSDPERCFSIQPEEGTHTTAPLDREA 180
DB 366 TVPENKAPGTLVGOISADLDSPASPPIRYISILPHSDPERCFSIQPEEGTHTTAPLDREA 425
QY 181 PAMNLTVLATL 193
DB 426 PAMNLTVLATL 438
RESULT 5
ADD29445
ID ADD29445 standard; protein; 636 AA.
AC ADD29445;
XX 15-JAN-2004 (first entry)
XX

```

```

DE Human cadherin-like protein amino acid sequence.
XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..16
XX Protein /label= Signal_peptide
XX /label= Mature_human_cadherin-like_protein
XX
XX US200314491-A1.
XX
XX 31-JUL-2003.
XX
XX 16-FEB-2001; 2001US-00788051.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX
XX (GODB/) GODBOLE S D.
XX (KUOC/) KUO C.
XX (ARTE/) ARTERBURN M C.
XX (YEUN/) YEUNG G.
XX (PALE/) PALENCIA S.
XX (TANG/) TANG Y T.
XX (LITC/) LIT C.
XX (DRMA/) DRMANAC R T.
XX
XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
XX Liu C, Drmanac RT;
XX
XX WPI; 2003-829799/77.
XX N-PSDB; ADD29461; ADD29446.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 4; 63pp; English.
XX
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of
XX transmembrane proteins which share a common cadherin domain in their
XX extracellular region. The extracellular portion mediates homotypic cell-
XX cell adhesion that is calcium dependent. Modulators of the protein of the
XX invention may have cytostatic or osteopathic activity. The invention may
XX allow development of therapeutics useful for the treatment of diseases
XX such as cancers, osteoporosis, Paget's disease, osteomalacia,
XX hyperostosis and osteopetrosis. The protein and DNA sequence of the
XX invention may also be useful as markers for prognosis of metastatic
XX tumours. The present sequence is that of the human secreted cadherin-like
XX protein of the invention.
SQ Sequence 636 AA;
Query Match 100.0%; Score 990; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4.2e-100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPCTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVQFSVETAGPCTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 321
QY 61 VRKPLDESGQSYSFREATNTLIDPAYLRGPFKVAVSVAVVQDAPPEPPTQAAVHL 120
DB 322 VRKPLDESGQSYSFREATNTLIDPAYLRGPFKVAVSVAVVQDAPPEPPTQAAVHL 381
QY 121 TVPENKAPGTLVGOISADLDSPASPPIRYISILPHSDPERCFSIQPEEGTHTTAPLDREA 180

```


Db 382 TYPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 441
 QY 181 RAMNNTLVATEL 193
 442 RAMNNTLVATEL 454

RESULT 6
 ABB53296
 ID ABB53296 standard; protein; 781 AA.

XX ABB53296;
 AC
 XX 12-FEB-2002 (first entry)

DE Human polypeptide #36.

XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquilizer; antiarrhythmic; cardiant; antidiabetic;
 KM antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
 KM nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-0203336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kadnick KS,

XX Lai Y, Xie Q;

XX WPI; 2002-041392/05.

XX N-PSDB; ABA96361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

XX PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

XX PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

XX Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,

XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,

XX 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,

XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as

XX given in the specification. The polypeptides, modulators of the

XX polypeptides and antibodies against the polypeptides are useful for

XX treating diseases such as neurological and psychiatric diseases including

XX Alzheimer's, parasympathetic palsy, Huntington's disease, myoclonic

XX dystrophy, anorexia and depression; cardiovascular diseases including

XX congestive heart failure, Hodgkin's disease and myocardial infarction;

XX respiratory diseases including asthma, chronic obstructive pulmonary

XX disease, cystic fibrosis and adult respiratory distress syndrome; liver

XX diseases including hypercholesterolaemia, cirrhosis, viral and nonviral

XX hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;

XX renal disease including renal failure, acute tubular necrosis and

XX glomerulonephritis; skeletal muscle diseases including Ehlers-Danlos

XX disease, hypoglycaemia and obesity; gastrointestinal diseases including

XX myocoma congenita and intestinal obstruction; lymph diseases including

XX lymphagiectasia; diseases of placenta including chorioarctomias; diseases

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

XX Query Match 100.0%; Score 990; DB 5; Length 781;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-100;

XX Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIXQSVVETAPGTLVGRTRAPDDLDNMLMAYSLIDGSEAFSTLDQGRDGLT 60

Db 262 SLIQSVVETAPGTLVGRTRAPDDLDNMLMAYSLIDGSEAFSTLDQGRDGLT 321

QY 61 VRKPLDFESQRSYSPVENTNTLIDPAYLRGPFKDVASVAVADAEPPAFTQAAVHL 120

Db 322 VRKPLDFESQRSYSPVENTNTLIDPAYLRGPFKDVASVAVADAEPPAFTQAAVHL 381

QY 121 TYPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 180

Db 382 TYPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 441

QY 181 RAMNNTLVATEL 193

Db 442 RAMNNTLVATEL 454

RESULT 7

AA48736

ID AA48736 standard; protein; 781 AA.

XX AA48736;

XX 28-MAR-2002 (first entry)

XX Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;

XX antidiabetic; neuroprotective; antiarrhythmic; antineumatic;

XX dermatological; immunosuppressive; antiinflammatory; antipruritic;

XX antidiabetic; antiallergic; antileptotic; haemostatic; antipruritic;

XX antithyroid; hypotensive; antiarteriosclerotic; cardiant; antiarrhythmic;

XX anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;

XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;

XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;

XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;

XX thrombus; inflammation; infection; ischaemia; irritabile bowel syndrome;

XX Gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016013.

XX 19-MAY-2000; 2000US-0205674P.

XX (MILL-) MILLENNITUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2002-083082/11.

XX N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for

XX diagnosing and treating disorders e.g. obstructive jaundice, multiple

XX sclerosis, encephalomyelitis and atherosclerosis and to identify

XX modulators of therapeutic use.

XX Claim 9; Page 105; 119pp; English.

PR 10-NOV-2000; 2000WO-US030873.

100 100 100

Dd 382 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441

Dd 382 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441

Db 442 RAMBLTVALTEL 454

RESULT 9

AD116606
ID AD116606 standard; protein, 781 AA.

XX AD116606;

DT 15-APR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions SegID142.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

KW inflammation; autoimmune disorder; allergy; blood disorder;

KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;

KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;

KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;

KW cytoskeletal; cardiac; antiinflammatory; immunosuppressive; antiallergic;

KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;

KW antiaesthetic; nephrotoxic; antiarthritic; hepatotoxic;

KW neuroprotective; nocitropic; antibacterial; virucide; antiparasitic;

KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;

XX chromosome mapping; tissue typing; pharmacogenomic.

XX Homo sapiens.

XX WO200268649-A2.

XX 06-SEP-2002.

XX 31-JAN-2002; 2002WO-US002785.

XX 31-JAN-2001; 2001US-0265395P.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 31-JAN-2001; 2001US-0265517P.

XX 02-FEB-2001; 2001US-0266406P.

XX 05-FEB-2001; 2001US-0266767P.

XX 07-FEB-2001; 2001US-0266975P.

XX 08-FEB-2001; 2001US-0267459P.

XX 09-FEB-2001; 2001US-0267823P.

XX 15-FEB-2001; 2001US-0268974P.

XX 26-FEB-2001; 2001US-0271664P.

XX 27-FEB-2001; 2001US-0271839P.

XX 27-FEB-2001; 2001US-0271855P.

XX 02-MAR-2001; 2001US-0272788P.

XX 14-MAR-2001; 2001US-0273925P.

XX 14-MAR-2001; 2001US-0275947P.

XX 14-MAR-2001; 2001US-0275950P.

XX 14-MAR-2001; 2001US-0275989P.

XX 14-MAR-2001; 2001US-0276448P.

XX 15-MAR-2001; 2001US-0276450P.

XX 16-MAR-2001; 2001US-0276397P.

XX 16-MAR-2001; 2001US-0276768P.

XX 20-MAR-2001; 2001US-0278552P.

XX 26-MAR-2001; 2001US-0278752P.

XX 26-MAR-2001; 2001US-0278778P.

XX 29-MAR-2001; 2001US-0279882P.

XX 29-MAR-2001; 2001US-0279884P.

XX 30-MAR-2001; 2001US-0280147P.

XX 11-APR-2001; 2001US-0282929P.

XX 11-APR-2001; 2001US-0283083P.

XX 20-APR-2001; 2001US-0285133P.

XX 23-APR-2001; 2001US-0285749P.

XX 03-MAY-2001; 2001US-0288327P.

XX 03-MAY-2001; 2001US-0288504P.

XX 29-MAY-2001; 2001US-0294047P.

XX 30-MAY-2001; 2001US-0294473P.

XX 08-JUN-2001; 2001US-0296964P.

PR 18-JUN-2001; 2001US-0296959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CURAGEN CORP.

XX Tchernov VT, Spyrek KA, Zerhusen BD, Patrurajan M, Shinkets RA;

PI Li L, Gangoli EA, Padigam M, Anderson DW, Rastelli L, Miller CE;

PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;

PI Furtak K, Grosse WM, Alsobrook JP, Lepley DW, Rieger DK, Burgess CE;

XX WPI; 2002-706998/76.

XX N-PSDB; AD116605.

XX New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

XX pharmacogenomics.

XX Claim 1; SEQ ID NO 142; 1498bp; English.

XX This invention relates to a novel nucleic acids, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for

CC diagnostic and prognostic assays and furthermore in the treatment of

CC diverse pathological conditions. The present invention describes novel

CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.

CC The NOVX polypeptides, polynucleotides and antibodies are useful in

CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,

CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in

CC treating or preventing diseases such as inflammation, autoimmune

CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome

CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,

CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

CC and epilepsy. Accordingly, these molecules have many activities including

CC cytoskeletal, cardiac, antiinflammatory, immunosuppressive, antiallergic,

CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,

CC antiaesthetic, nephrotoxic, antiarthritic, hepatotoxic,

CC neuroprotective, nocitropic, antibacterial, virucide, antiparasitic,

CC relaxant and anticonvulsant. In addition, they are useful in screening

CC assays to identify small molecules that modulate or inhibit, for example,

CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. This polypeptide is a human NOVX protein of the

XX invention.

XX Sequence 781 AA;

Query Match 100.0%; Score 990; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 5.6e-100; Indels 0; Gaps 0;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGTIGRGLRQDPDLGNALMAYSILIDGESSEAFSISTDQGRGLLT 60

Db 262 SLVQFSVETAGPGTIGRGLRQDPDLGNALMAYSILIDGESSEAFSISTDQGRGLLT 321

QY 61 VRKPLDFESQRSYSFVEVATNTLIDPAYLRGPGKQVAVAVADAPPPTQAAYHL 120

Db 322 VRKPLDFESQRSYSFVEVATNTLIDPAYLRGPGKQVAVAVADAPPPTQAAYHL 381

QY 121 TYPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCPSIOPEGTHHTAAPLDREA 180
DB 382 TYPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCPSIOPEGTHHTAAPLDREA 441
CY 181 RAMNLT/LATEL 193
DB 442 RAMNLT/LATEL 454

RESULT 10
ABR40114
ID ABR40114 standard; protein; 781 AA.
XX ABR40114;
AC ABR40114;
DT 04-JUL-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein, CADECM-11.
XX
KW Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
KW anticonvulsant; neurotrophic; neuroprotective; immunosuppressive;
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KW gene therapy; cell adhesion; extracellular matrix; CADECM;
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
KW atherosclerosis.

OS Homo sapiens.
XX
XX WO2003027230-A2.
XX
XX 03-APR-2003.
XX
XX 02-AUG-2002; 2002WO-US024649.
XX
XX 03-AUG-2001; 2001US-030964P.
XX 03-AUG-2001; 2001US-031019P.
XX 17-AUG-2001; 2001US-0313091P.
XX 31-AUG-2001; 2001US-0316771P.
XX 07-SEP-2001; 2001US-0317896P.
XX 21-SEP-2001; 2001US-0324781P.
XX 05-OCT-2001; 2001US-0327606P.
XX 12-OCT-2001; 2001US-0328960P.
XX 09-NOV-2001; 2001US-0344471P.
XX 17-MAY-2002; 2002US-0381291P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
XX Forsythe J, Elliott VS, Griffith JA, Gervad AE, Azimzai Y,
XX Kalliock DA, Xu Y, Honchel CD, Baughn MR, Gietzen KJ, Lee S,
XX Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX WPI; 2003-354645/33.
XX
XX N-PSDB; ACC00402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
XX useful for diagnosing, treating or preventing disorders associated with
XX aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX or stroke.
XX
XX
XX Claim 1; Page 192-194; 234pp; English.

CC The present invention relates to novel human cell adhesion and
CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
CC and proteins are useful in diagnosing, treating and preventing disorders
CC associated with aberrant expression of CADECM, such as immune system
CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's

CC syndrome or cerebral palsy); connective tissue disorders (e.g. systemic
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
CC proliferative disorders (e.g. cancer or atherosclerosis)
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100; Mismatches 0; Gaps 0;
Matches 193; Conservative 0; Indels 0;

QY 1 SLYQFSVETAGPGLVGRRAQDDPDLGDNALMAYSLIDGSGSAFISITDLOCRDGLT 60
DB 262 SLYQFSVETAGPGLVGRRAQDDPDLGDNALMAYSLIDGSGSAFISITDLOCRDGLT 321
QY 61 VKKPLDFESQSRYSFRVATNTLIDPAVLRGPFKDVASVVAQDAPPEPAFQAAYHL 120
DB 322 VKKPLDFESQSRYSFRVATNTLIDPAVLRGPFKDVASVVAQDAPPEPAFQAAYHL 381
QY 121 TYPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCPSIOPEGTHHTAAPLDREA 180
DB 382 TYPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCPSIOPEGTHHTAAPLDREA 441
QY 181 RAMNLT/LATEL 193
DB 442 RAMNLT/LATEL 454

RESULT 11
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
XX ADA01366;
AC ADA01366;
DT 06-NOV-2003 (first entry)
XX
XX Human PRO polypeptide #49.
XX
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

OS Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gunney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-625484/59.
XX
XX N-PSDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX
XX Claim 11; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and

transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO factor-alpha (TGF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100; Mismatches 0; Gaps 0;
Matches 193; Conservative 0; Indels 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSILDGSESEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSILDGSESEAFSISTDLQGRDGLT 321
QY 61 VRKPLDPSQSRYSFRVEATNTLLDPAYLRGPRKDVASVRVAVQDAPEPPAFQAAYHL 120
Db 322 VRKPLDPSQSRYSFRVEATNTLLDPAYLRGPRKDVASVRVAVQDAPEPPAFQAAYHL 381
QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
Db 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAWNLTVLATEL 193
Db 442 RAWNLTVLATEL 454

RESULT 12

ADA43795
ID ADA43795 standard; protein; 781 AA.

XX ADA43795;
XX AC
XX 20-NOV-2003 (first entry)
XX DT

XX Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.

XX Homo sapiens.

XX US2003064474-A1.

XX 03-APR-2003.

XX 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027039.
XX PR 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2003-605867/57.
XX N-PSDB; ADA43794.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
XX PRO21383, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.

PS Claim 11; Fig 98; 308pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
XX and PRO21383 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.

Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100; Mismatches 0; Gaps 0;
Matches 193; Conservative 0; Indels 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSILDGSESEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSILDGSESEAFSISTDLQGRDGLT 321
QY 61 VRKPLDPSQSRYSFRVEATNTLLDPAYLRGPRKDVASVRVAVQDAPEPPAFQAAYHL 120
Db 322 VRKPLDPSQSRYSFRVEATNTLLDPAYLRGPRKDVASVRVAVQDAPEPPAFQAAYHL 381
QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
Db 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAWNLTVLATEL 193
Db 442 RAWNLTVLATEL 454

RESULT 13

ADA43563
ID ADA43563 standard; protein; 781 AA.

ADA43563;
 20-NOV-2003 (first entry)
 Human secreted/transmembrane polypeptide PRO34009.
 Human, PRO; secreted protein; transmembrane protein;
 endothelial cell tube formation; chondrocyte cell differentiation;
 microvascular endothelial cell; tumour; lung tumour; colon tumour;
 breast tumour; prostate tumour; rectal tumour; kidney tumour;
 liver tumour; cytostatic; vaccine.
 Homo sapiens.
 US2003073196-A1.
 17-APR-2003.
 18-SEP-2002; 2002US-00246210.
 04-APR-2001; 2001US-0282199P.
 29-AUG-2001; 2001WO-US027099.
 18-JUL-2002; 2002US-00197942.
 (GETH) GENENTECH INC.
 Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 Fong S;
 WPI: 2003-743814/70.
 N-PSDB; ADA43562.
 New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PRO21383 useful for stimulating the proliferation or differentiation of
 chondrocyte cells and detecting the presence of a tumor in a mammal.
 Claim 11; Fig 98; 307pp; English.

The invention relates to an isolated secreted/transmembrane (PRO)
 polypeptide, having at least 80% sequence identity to a sequence selected
 from any one of the 57 amino acid sequences given in specification, or to
 a sequence encoded by a nucleic acid molecule selected from any one of
 the nucleic acids deposited under any of the ATCC accession numbers given
 in specification, or a sequence having at least 80% identity to PRO
 lacking its associated signal peptide, an extracellular domain of PRO
 with or without its associated signal peptide. Also included are vectors,
 transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 administering PRO281, PRO1560, PRO189, PRO449, PRO6308, PRO6000,
 PRO10275, PRO20933 or PRO34274 polypeptide or its agonist) and
 an oligonucleotide probe derived from any one of the above nucleotide
 sequences. PRO6018 polypeptide is useful for stimulating the
 proliferation or differentiation of chondrocyte cells. PRO133, PRO20080
 and PRO21383 polypeptides are useful for stimulating the proliferation of
 human microvascular endothelial cells. PRO6071, PRO487 and PRO6006
 polypeptides are useful for inhibiting the proliferation of human
 microvascular endothelial cells. PRO polypeptides are useful for
 detecting the presence of tumour in a mammal, including tumours of lung,
 colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 PRO189, PRO449, PRO6308, PRO6000, PRO10275, PRO21297, PRO20933 and
 PRO34274 polypeptides are useful for inducing endothelial cell tube
 formation. PRO or the antibody are useful in the preparation of a
 medicament for treating a condition responsive to PRO polypeptide. The
 oligonucleotide probes are useful for isolating genomic and cDNA
 nucleotide sequences, for measuring or detecting the expression of an
 associated gene, and as antisense probes. PRO nucleic acid is useful as a
 hybridisation probe, in chromosome and gene mapping, in the generation of
 antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 present sequence represents a PRO protein.

Sequence 781 AA;

Query Match 100.0%; Score 990; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5,6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVPSVETAGPGTLVLRRAQDPDLGDNLAAVSTLDGSGSAFSTLDLQGRDGLT 60
 DB 262 SLVPSVETAGPGTLVLRRAQDPDLGDNLAAVSTLDGSGSAFSTLDLQGRDGLT 321
 QY 61 VRKPLDFESQASYSFRRVATNTLIDPAYLRGPFKDVASVAVQDAPPEPAFQAAYHL 120
 DB 322 VRKPLDFESQASYSFRRVATNTLIDPAYLRGPFKDVASVAVQDAPPEPAFQAAYHL 381
 QY 121 TYPENKAPGTLVGOISAADLDSPASPIRYSILPHSPDPERGFSIQPEEGTHTAAPLDREA 180
 DB 382 TYPENKAPGTLVGOISAADLDSPASPIRYSILPHSPDPERGFSIQPEEGTHTAAPLDREA 441
 QY 181 RAMHNLTVLATEL 193
 DB 442 RAMHNLTVLATEL 454

RESULT 14
 ADA01238
 ID ADA01238 standard; protein; 781 AA.
 AC ADA01238;
 AC 06-NOV-2003 (first entry)
 DT Human PRO polypeptide #49.
 DE Human PRO polypeptide #49.
 DE Human, PRO; secreted polypeptide; transmembrane polypeptide;
 tumour necrosis factor-alpha; TNF-alpha blood; chondrocyte cell; tumour;
 cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 microvascular endothelial cell; endothelial cell tube formation.
 OS Homo sapiens.
 XX US2003068782-A1.
 XX 10-APR-2003.
 XX 16-SEP-2002; 2002US-00245851.
 XX 27-APR-1999; 99US-0131271P.
 XX 29-OCT-1999; 99US-0162506P.
 XX 02-DEC-1999; 99WO-US028551.
 XX 29-AUG-2001; 2001WO-US027099.
 XX 18-JUL-2002; 2002US-00197942.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 XX Fong S;
 XX WPI: 2003-625487/59.
 XX N-PSDB; ADA01237.
 XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 XX preparation of a medicament for treating a condition responsive to PRO
 XX polypeptide, and as therapeutic agents e.g. vaccines.
 XX Claim 11; Fig 98; 308pp; English.

The invention relates to isolated human PRO polypeptides (secreted and
 transmembrane polypeptides) and the polynucleotides encoding them. The
 invention also relates to an antibody which specifically binds to a PRO
 polypeptide, a method for stimulating the release of tumour necrosis
 factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 proliferation or differentiation of chondrocyte cells and a method for
 detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,

CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.

SO Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDEGSEAFSISTDLOGRDGLLT 60
 DB 262 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDEGSEAFSISTDLOGRDGLLT 321
 QY 61 VRKPLDFESQRSYSFRVEANTLTLDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
 DB 322 VRKPLDFESQRSYSFRVEANTLTLDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 381
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
 QY 181 RAWENLTVALTEL 193
 DB 442 RAWENLTVALTEL 454

RESULT 15

ADA01122
 ID ADA01122 standard; protein; 781 AA.

XX ADA01122;

DT 06-NOV-2003 (first entry)

DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytosol; vaccine.

XX Homo sapiens.

XX US2003068780-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245143.

XX 02-AUG-2000; 2000US-0222695P.

XX 20-JUN-2001; 2001WO-US019692.

XX 29-AUG-2001; 2001WO-US027039.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Batton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Guirney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S,
 XX WPI; 2003-625485/59.

DR N-PSDB; ADA01121.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 11; Fig 98; 307pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO313, PRO20080
 CC and PRO3133 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.

SO Sequence 781 AA:

Query Match 100.0%; Score 990; DB 7; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDEGSEAFSISTDLOGRDGLLT 60
 DB 262 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDEGSEAFSISTDLOGRDGLLT 321
 QY 61 VRKPLDFESQRSYSFRVEANTLTLDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
 DB 322 VRKPLDFESQRSYSFRVEANTLTLDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 381
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
 QY 181 RAWENLTVALTEL 193
 DB 442 RAWENLTVALTEL 454

Search completed: December 8, 2004, 10:13:07
 Job time : 80.866 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 197.215 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990

Sequence: 1 SLVQFSVETAGPCTLVGRLL.....APDREARAHNTVLTATL 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	990	100.0	193	US-09-788-051-15
2	990	100.0	493	US-10-072-012-482
3	990	100.0	607	US-10-258-951-74
4	990	100.0	620	US-09-788-051-7
5	990	100.0	636	US-09-788-051-4
6	990	100.0	781	US-09-860-868-2
7	990	100.0	781	US-10-245-752-98
8	990	100.0	781	US-10-245-859-98
9	990	100.0	781	US-10-245-103-98
10	990	100.0	781	US-10-245-107-98
11	990	100.0	781	US-10-245-143-98
12	990	100.0	781	US-10-245-771-98
13	990	100.0	781	US-10-245-851-98

14	990	100.0	781	US-10-245-883-98	Sequence 98, Appl
15	990	100.0	781	US-10-237-535-98	Sequence 98, Appl
16	990	100.0	781	US-10-238-183-98	Sequence 98, Appl
17	990	100.0	781	US-10-238-283-98	Sequence 98, Appl
18	990	100.0	781	US-10-238-370-98	Sequence 98, Appl
19	990	100.0	781	US-10-245-055-98	Sequence 98, Appl
20	990	100.0	781	US-10-245-147-98	Sequence 98, Appl
21	990	100.0	781	US-10-245-730-98	Sequence 98, Appl
22	990	100.0	781	US-10-245-739-98	Sequence 98, Appl
23	990	100.0	781	US-10-246-210-98	Sequence 98, Appl
24	990	100.0	781	US-10-239-196-98	Sequence 98, Appl
25	990	100.0	781	US-10-243-024-98	Sequence 98, Appl
26	990	100.0	781	US-10-243-409-98	Sequence 98, Appl
27	990	100.0	781	US-10-245-621-98	Sequence 98, Appl
28	990	100.0	781	US-10-245-860-98	Sequence 98, Appl
29	990	100.0	781	US-10-245-033-98	Sequence 98, Appl
30	990	100.0	781	US-10-243-095-98	Sequence 98, Appl
31	990	100.0	781	US-10-245-185-98	Sequence 98, Appl
32	990	100.0	781	US-10-245-447-98	Sequence 98, Appl
33	990	100.0	781	US-10-245-473-98	Sequence 98, Appl
34	990	100.0	781	US-10-245-770-98	Sequence 98, Appl
35	990	100.0	781	US-10-245-877-98	Sequence 98, Appl
36	990	100.0	781	US-10-246-976-98	Sequence 98, Appl
37	990	100.0	781	US-10-243-320-98	Sequence 98, Appl
38	990	100.0	781	US-10-162-445-13	Sequence 13, Appl
39	990	100.0	781	US-10-242-743-98	Sequence 98, Appl
40	990	100.0	781	US-10-242-845-98	Sequence 98, Appl
41	990	100.0	781	US-10-237-865-98	Sequence 98, Appl
42	990	100.0	781	US-10-238-325-98	Sequence 98, Appl
43	990	100.0	781	US-10-238-346-98	Sequence 98, Appl
44	990	100.0	781	US-10-238-411-98	Sequence 98, Appl
45	990	100.0	781	US-10-243-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-15
Sequence 15, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y Tom
APPLICANT: Lau, Chenghua
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT FILING DATE: 2001-02-16
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-15

Query Match 100.0%; Score 990; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 2, 2e-89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SLVQFSVETAGPCTLVGRLLRAQDPDLGNALMAYSLDGGSEAFISTDQSGDGLT 60

Db 1 SLVGSFVETAGPGLVGRRAQDPDLDGNALMAYSLDDEGSEAFSISTDLQGRDGLT 60
Qy 61 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 120
Db 61 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 120
Qy 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Qy 181 RAMNLTVLATL 193
Db 181 RAMNLTVLATL 193

RESULT 2
US-10-072-482
Sequence 482, Application US/10072012
Publication No. US2004003493A1

GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zethusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimyr Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsbrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieser, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 482
LENGTH: 493
TYPE: PRT

ORGANISM: Homo sapiens
US-10-072-012-482
Query Match 100.0%; Score 990; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 7,9e-89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLVGSFVETAGPGLVGRRAQDPDLDGNALMAYSLDDEGSEAFSISTDLQGRDGLT 60
Db 262 SLVGSFVETAGPGLVGRRAQDPDLDGNALMAYSLDDEGSEAFSISTDLQGRDGLT 321
Qy 61 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 120
Db 322 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 381
Qy 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 382 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
Qy 181 RAMNLTVLATL 193
Db 442 RAMNLTVLATL 454

RESULT 3
US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US2004003504A1
GENERAL INFORMATION:
APPLICANT: Mardwal, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Zhaoying F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GRS0025
CURRENT APPLICATION NUMBER: US/10/258,951
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 990; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLVGSFVETAGPGLVGRRAQDPDLDGNALMAYSLDDEGSEAFSISTDLQGRDGLT 60
Db 262 SLVGSFVETAGPGLVGRRAQDPDLDGNALMAYSLDDEGSEAFSISTDLQGRDGLT 321
Qy 61 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 120
Db 322 VRKPLDFESQSRYSFRVEATNTLLDPAYLRGPKDVASVRVAVQDAPEPPAFQAAYHL 381
Qy 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180

Db 382 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
Db 442 RAMHNLTVLATEL 454

RESULT 4

US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Attezburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 990; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 60
Db 246 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 305
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
Db 306 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 365
QY 121 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 366 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 425
QY 181 RAMHNLTVLATEL 193
Db 426 RAMHNLTVLATEL 438

RESULT 5

US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Attezburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 990; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 60
Db 262 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 321
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
Db 322 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 382 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
Db 442 RAMHNLTVLATEL 454

RESULT 6

US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 990; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 60
Db 262 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLOGRDGLLT 321
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
Db 322 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 382 TVPENKAGTLVGIQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441

OY 181 RAMNLTIVLATEL 193
DB 442 RAMNLTIVLATEL 454

RESULT 7

US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

Query Match 100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SLVPSVETAGPGTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVPSVETAGPGTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 321
OY 61 VRKPLDFESQSYFRRVETATNTLIDPAYLRGPKDVASVAVAVQDAPPEPAFTQAAYHL 120
DB 322 VRKPLDFESQSYFRRVETATNTLIDPAYLRGPKDVASVAVAVQDAPPEPAFTQAAYHL 381
OY 121 TVPENKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
DB 382 TVPENKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 441
OY 181 RAMNLTIVLATEL 193

DB 442 RAMNLTIVLATEL 454

RESULT 8

US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match 100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SLVPSVETAGPGTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVPSVETAGPGTLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRDGLLT 321
OY 61 VRKPLDFESQSYFRRVETATNTLIDPAYLRGPKDVASVAVAVQDAPPEPAFTQAAYHL 120
DB 322 VRKPLDFESQSYFRRVETATNTLIDPAYLRGPKDVASVAVAVQDAPPEPAFTQAAYHL 381
OY 121 TVPENKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
DB 382 TVPENKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 441
OY 181 RAMNLTIVLATEL 193
DB 442 RAMNLTIVLATEL 454

```
RESULT 9
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wacande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 60
DB 262 SLVQFSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 321
QY 61 VRKPLDFESQRSYFRVAVATNTLIDPAYLRGPFQDVASVRVAQDAPEPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYFRVAVATNTLIDPAYLRGPFQDVASVRVAQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEGTHTAAPLDREA 180
DB 382 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
DB 442 RAMHNLTVLATEL 454

RESULT 10
```

```
US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wacande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match          100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 60
DB 262 SLVQFSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 321
QY 61 VRKPLDFESQRSYFRVAVATNTLIDPAYLRGPFQDVASVRVAQDAPEPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYFRVAVATNTLIDPAYLRGPFQDVASVRVAQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEGTHTAAPLDREA 180
DB 382 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
DB 442 RAMHNLTVLATEL 454

RESULT 11
US-10-245-143-98
; Sequence 98, Application US/10245143
```

```

PUBLICatioN No.: US2003068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSERRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C90
CURRENT FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 1997-09-17
PRIORITY FILING DATE: 60/063046
PRIORITY FILING DATE: 1997-10-24
PRIORITY APPLICATION NUMBER: 60/065027
PRIORITY FILING DATE: 1997-11-10
PRIORITY APPLICATION NUMBER: 60/079689
PRIORITY FILING DATE: 1998-03-27
PRIORITY APPLICATION NUMBER: 60/086478
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: 60/087607
PRIORITY FILING DATE: 1998-06-02
PRIORITY APPLICATION NUMBER: 60/089801
PRIORITY FILING DATE: 1998-06-18
PRIORITY APPLICATION NUMBER: 60/090557
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090689
PRIORITY FILING DATE: 1998-06-25
REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRF
ORGANISM: Homo Sapien
US-10-245-143-98
Query Match          100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,5e+88;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      1 SLVQSVETAGPGTLVGRALRAQDDLDGNLMAYSILIDGGSGAFSISTDLGRCGLIT 60
DB      262 SLVQSFVVTAGTGLTVGRALRAQDDLDGNLMAYSLIDGGSGAFSISTDLGRCGLIT 321
QY      61 VRKPLFEESQRASSTFFVEATNTLLIDPAYLRGPCKDVASRVAAVDAPPEPATQAAYHL 120
DB      322 VRKPLDFEESQRSRRVAETNTLLIDPAYLRGPCKDVASRVAAVDAPPEPATQAAYHL 381
QY      121 TVENKAPEGTLVGQISADLDSPASPIRYSLIPSDPERCFSTIQEEGTHTAAPLDREA 180
DB      382 TVENKAPEGTLVGQISADLDSPASPIRYSLIPSDPERCFSTIQEEGTHTAAPLDREA 441
QY      181 RAWHNLTVLATEL 193
DB      442 RAWHNLTVLATEL 454
RESULT 12
US-10-245-771-98
Sequence 98, Application US/10245771
Publication No.: US20030068781A1
GENERAL INFORMATION:

```

```

1 APPLICANT: Baker, Kevin
2 APPLICANT: Eaton, Dan
3 APPLICANT: Filvaroff, Ellen
4 APPLICANT: Goddard, Audrey
5 APPLICANT: Grimaldi, J. Christopher
6 APPLICANT: Guirney, Austin
7 APPLICANT: Smith, Victoria
8 APPLICANT: Stephan, Jean-Phillippe
9 APPLICANT: Matanhe, Colin
10 APPLICANT: Wood, William
11 APPLICANT: Zhang, Zemin
12 APPLICANT: Fong, Sherman
13 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
14 FILE REFERENCE: P3630R1C98
15 CURRENT APPLICATION NUMBER: US/10/245,771
16
17 PRIOR FILING DATE: 2002-09-16
18 PRIOR APPLICATION NUMBER: 10/197942
19 PRIOR FILING DATE: 2002-07-18
20 PRIOR APPLICATION NUMBER: 60/059114
21 PRIOR FILING DATE: 1997-09-17
22 PRIOR APPLICATION NUMBER: 60/063046
23 PRIOR FILING DATE: 1997-10-24
24 PRIOR APPLICATION NUMBER: 60/065027
25 PRIOR FILING DATE: 1997-11-10
26 PRIOR APPLICATION NUMBER: 60/079689
27 PRIOR FILING DATE: 1998-03-27
28 PRIOR APPLICATION NUMBER: 60/086478
29 PRIOR FILING DATE: 1998-05-22
30 PRIOR APPLICATION NUMBER: 60/087607
31 PRIOR FILING DATE: 1998-06-02
32 PRIOR APPLICATION NUMBER: 60/089601
33 PRIOR FILING DATE: 1998-06-18
34 PRIOR APPLICATION NUMBER: 60/090557
35 PRIOR FILING DATE: 1998-06-24
36 PRIOR APPLICATION NUMBER: 60/090689
37 PRIOR FILING DATE: 1998-06-25
38 Remaining Prior Application data removed - See File Wrapper or PALM.
39 NUMBER OF SEQ ID NOS: 116
40
41 SEQ ID NO 98
42
43 LENGTH: 781
44 TYPE: PRT
45 ORGANISM: Homo Sapien
46
47 US-10-245-771-98
48
49 Query Match 100.0%; Score 990; DB 14; Length 781;
50 Best Local Similarity 100.0%; Pred. No. 1,5e-86;
51 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0
52
53 QY 1 SLTQSFVNTAGBGLTVGLRQADPDLDGNLMAYSLIDGSGSEAFSISTDQGRDGLT 60
54 DB 262 SLTQSFVNTAGBGLTVGLRQADPDLDGNLMAYSLIDGSGSEAFSISTDQGRDGLT 322
55 QY 61 VRKPLDFEORSYSPFEVNTNTLIDPAYLRQPFKDVAVFVAVQDAPEPPAFTQAAVYL 120
56 DB 322 VRKPLDFEORSYSPFEVNTNTLIDPAYLRQPFKDVAVFVAVQDAPEPPAFTQAAVYL 381
57 QY 121 TVPENKAPEGLTVQGISADLDSPAPPIRYSLPHSDPFRCTSIQPEEGTITTAFLPREA 180
58 DB 382 TVPENKAPEGLTVQGISADLDSPAPPIRYSLPHSDPFRCTSIQPEEGTITTAFLPREA 441
59 QY 181 RAWHNLTVLATEL 193
60 DB 442 RAWHNLTVLATEL 454
61
62 RESULT 13
63 US-10-245-851-98
64 ; Sequence 98, Application US/10245851
65 ; Publication No. US20030068782A1
66 GENERAL INFORMATION:
67 APPLICANT: Baker, Kevin
68 APPLICANT: Eaton, Dan

```


APPLICANT: Smith,Victoria
APPLICANT: Stephan,Jean-Philippe
APPLICANT: Watanabe,Colin
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C3
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US/10/237,535
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/152228
PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-06
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/22896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129

;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/282199
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/290589
;; PRIOR FILING DATE: 2001-05-09
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/267213
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-09
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 10/001054
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/081056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 10/119480
;; PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 990; DB 14; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVPSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGEGSAFISITDLCGRDGLT 60
DB 262 SLVGSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGEGSAFISITDLCGRDGLT 321
QY 61 VRKPLDFESORSYSRVRATNTLLIDPAYLRGPFKDVASVRVAQDAPEPAFTQAAVHL 120
DB 322 VRKPLDFESORSYSRVRATNTLLIDPAYLRGPFKDVASVRVAQDAPEPAFTQAAVHL 381
QY 121 TVPENKAPGLTVGQISAADLDSAPSPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
DB 382 TVPENKAPGLTVGQISAADLDSAPSPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAMENLTVLATEL 193
DB 442 RAMENLTVLATEL 454

This Page Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 23.0142 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVQFSVETAGPGLVGR.....APLDREARAHNLTVALTEL 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	54.5	693	2	US-08-738-349-6 Sequence 6, Appli
2	540	54.5	693	4	US-09-918-497-55 Sequence 5, Appli
3	540	54.5	796	2	US-08-738-349-4 Sequence 4, Appli
4	537	54.2	796	1	US-08-188-228-58 Sequence 58, Appli
5	537	54.2	796	1	US-08-332-643-52 Sequence 52, Appli
6	537	54.2	796	1	US-08-332-643-58 Sequence 58, Appli
7	537	54.2	796	4	US-09-654-328-2 Sequence 2, Appli
8	532	53.7	796	2	US-08-738-349-2 Sequence 2, Appli
9	522	52.7	532	1	US-08-188-228-44 Sequence 44, Appli
10	522	52.7	532	1	US-08-332-638-44 Sequence 44, Appli
11	522	52.7	799	1	US-08-188-228-42 Sequence 42, Appli
12	522	52.7	799	1	US-08-332-638-42 Sequence 42, Appli
13	521	52.6	793	1	US-08-188-228-54 Sequence 54, Appli
14	521	52.6	793	1	US-08-332-643-48 Sequence 48, Appli
15	521	52.6	793	1	US-08-332-638-54 Sequence 54, Appli
16	459	45.4	653	1	US-08-188-228-46 Sequence 46, Appli
17	447	45.2	653	1	US-08-332-638-46 Sequence 46, Appli
18	447	45.2	615	2	US-08-738-349-12 Sequence 12, Appli
19	407	41.1	794	1	US-08-188-228-60 Sequence 60, Appli
20	407	41.1	794	1	US-08-332-643-54 Sequence 54, Appli
21	407	41.1	794	1	US-08-332-638-50 Sequence 50, Appli
22	314.5	31.8	780	1	US-08-188-228-50 Sequence 50, Appli
23	314.5	31.8	780	1	US-08-332-643-44 Sequence 44, Appli
24	314.5	31.8	780	1	US-08-332-638-50 Sequence 50, Appli
25	203	20.5	712	2	US-08-474-067-2 Sequence 5, Appli
26	203	20.5	712	2	US-08-474-067-5 Sequence 5, Appli
27	203	20.5	712	2	US-08-474-068A-2 Sequence 2, Appli

28	203	20.5	712	2	US-08-474-068A-5	Sequence 5, Appli
29	203	20.5	712	2	US-08-472-481-2	Sequence 2, Appli
30	203	20.5	717	2	US-08-474-067-4	Sequence 4, Appli
31	203	20.5	717	2	US-08-474-068A-4	Sequence 4, Appli
32	203	20.5	717	2	US-08-472-481-4	Sequence 7, Appli
33	200	20.2	837	2	US-08-474-067-7	Sequence 7, Appli
34	200	20.2	837	2	US-08-474-068A-7	Sequence 6, Appli
35	200	20.2	837	2	US-08-472-481-6	Sequence 6, Appli
36	198.5	20.1	713	1	US-08-188-228-62	Sequence 56, Appli
37	198.5	20.1	713	1	US-08-332-643-56	Sequence 62, Appli
38	198.5	20.1	713	1	US-08-332-638-62	Sequence 95, Appli
39	198.5	20.1	1026	1	US-07-998-003A-95	Sequence 95, Appli
40	198.5	20.1	1026	1	US-08-453-274B-95	Sequence 95, Appli
41	198.5	20.1	1026	1	US-08-453-695A-95	Sequence 95, Appli
42	198.5	20.1	1026	1	US-08-268-161A-95	Sequence 95, Appli
43	198.5	20.1	1026	2	US-08-453-702A-95	Sequence 95, Appli
44	198.5	20.1	1026	3	US-09-099-639-95	Sequence 95, Appli
45	198.5	20.1	1026	5	PCT-US93-12588-95	Sequence 95, Appli

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sumao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Teshimura, Atsushi
APPLICANT: Amano, Egon
TITLE OR INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 54.5%; Score 540; DB 2; Length 693;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAYSLDGESEAFSISTDLQGRDLT 60
DB 271 SVYQISVEAAVPEEVEGRVAKDPDIDGKLVYINIVDDGMSFEITTDYEQGVIX 330
QY 61 VRKPLDEFSQSYSFVREATNTLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAYSLKVEAAVHIDPKFISNGPFKDVYKIAVEDADEPMLASVYH 390
QY 121 TVPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENAAAGTVGVGVHAKDPDANSPIRYSIDRHTLDRFETINPEDGFKITKPLDREE 450
QY 181 RAWNLTVLATEL 193
DB 451 TAWNLITVFAAEI 463

RESULT 2

US-09-919-497-55
; Sequence 55, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutecr, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 66/221,735
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 54.5%; Score 540; DB 4; Length 693;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAYSLDGESEAFSISTDLQGRDLT 60
DB 271 SVYQISVEAAVPEEVEGRVAKDPDIDGKLVYINIVDDGMSFEITTDYEQGVIX 330
QY 61 VRKPLDEFSQSYSFVREATNTLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAYSLKVEAAVHIDPKFISNGPFKDVYKIAVEDADEPMLASVYH 390
QY 121 TVPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENAAAGTVGVGVHAKDPDANSPIRYSIDRHTLDRFETINPEDGFKITKPLDREE 450
QY 181 RAWNLTVLATEL 193
DB 451 TAWNLITVFAAEI 463

RESULT 3
US-08-738-349-4
; Sequence 4, Application US/08738349
; Patent No. 5869638
; GENERAL INFORMATION:
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Kawai, Shinji
; APPLICANT: Tsujimura, Akiyoshi
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Cadherin-like Protein and

TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 54.5%; Score 540; DB 2; Length 796;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLDGNALMAYSLDGESEAFSISTDLQGRDLT 60
DB 271 SVYQISVEAAVPEEVEGRVAKDPDIDGKLVYINIVDDGMSFEITTDYEQGVIX 330
QY 61 VRKPLDEFSQSYSFVREATNTLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAYSLKVEAAVHIDPKFISNGPFKDVYKIAVEDADEPMLASVYH 390
QY 121 TVPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENAAAGTVGVGVHAKDPDANSPIRYSIDRHTLDRFETINPEDGFKITKPLDREE 450
QY 181 RAWNLTVLATEL 193
DB 451 TAWNLITVFAAEI 463

RESULT 4
US-08-188-228-58
; Sequence 58, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shin-iro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Garstein, Murray &
; ADDRESSEE: Borum
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query March 54.2%; Score 537; DB 1; Length 796;
Best Local Similarity 51.6%; Pred. No. 3.1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVVETAGPTLVGRRAQDPDLGDNALMAYSLDGGSEAFSISTDLQGRGLTV 61
DB 272 LYQSVSEAAVPGEEVGRVAKDPDIGNGLVTYNIVDGMESFEITTDYETORGVIKL 331
QY 62 RKPDLFESQRSYFRVEATNTLIDPAYLRGPFQDVASVRAVODAPPEPAFTQAAVHLT 121
DB 332 KKPVDFTERRAYSLEKVEANVHIDPKFISNGPFKDTLVKISVEDADEPPEFLASVYHE 391
QY 122 VPEKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFISIOPEEGTHTAPLDREAR 181
DB 392 VQENAAAGTVGRVAKDPDANSPIRYSIDRHTDLDRFFITNPEDEGFIKTKRLDREBT 451

QY 182 AMHNLTVLATEL 193
DB 452 AMNLTVFAAEI 463

RESULT 5
US-08-332-643-52
Sequence 52, Application US/08332643
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 563963and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query March 54.2%; Score 537; DB 1; Length 796;
Best Local Similarity 51.6%; Pred. No. 3.1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVVETAGPTLVGRRAQDPDLGDNALMAYSLDGGSEAFSISTDLQGRGLTV 61
DB 272 LYQSVSEAAVPGEEVGRVAKDPDIGNGLVTYNIVDGMESFEITTDYETORGVIKL 331
QY 62 RKPDLFESQRSYFRVEATNTLIDPAYLRGPFQDVASVRAVODAPPEPAFTQAAVHLT 121
DB 332 KKPVDFTERRAYSLEKVEANVHIDPKFISNGPFKDTLVKISVEDADEPPEFLASVYHE 391
QY 122 VPEKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFISIOPEEGTHTAPLDREAR 181
DB 392 VQENAAAGTVGRVAKDPDANSPIRYSIDRHTDLDRFFITNPEDEGFIKTKRLDREBT 451

QY 182 AMHNLTVLATEL 193
DB 452 AMNLTVFAAEI 463

RESULT 6
US-08-332-638-58
Sequence 58, Application US/08332638
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 54.2%; Score 537; DB 1; Length 796;
Best Local Similarity 51.6%; Pred. No. 3,1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVVETAGPGLVGRRLAOPDDGDNALMAYSILIDGSGSAFISITDLOGRDGLTV 61
DB 272 LYQMSVSEAAPGSEVGRVAKADPDIGENGLVTYNIIVDGGMESFELTDTYETQSGVTKL 331
QY 62 RKPLDFESQSRYSFRVEATNTLIDPAYLRGPFKCVASVAVQADAPPPAFQAAHYHL 121
DB 332 KKPVDFFETERYASLKVEAAVNHIDPKFISNGPFKDTVTVKISVEDDEPMPFLAPSYIHE 391
QY 122 VPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIOEEGTIHTAPLDREAR 181
DB 392 VQENAAAGTVGRVHADPDPAANSPIRYSIDRHTDLDREFTINPDGFIKTTKPLDREFT 451
QY 182 AMNLTIVLATEL 193
DB 452 AMNLTIVFAAEI 463

RESULT 7
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
TITLE OF INVENTION: Methods and Compositions for Treatment
OF INFLAMMATORY Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/ERE/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 54.2%; Score 537; DB 4; Length 796;
Best Local Similarity 51.6%; Pred. No. 3,1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVVETAGPGLVGRRLAOPDDGDNALMAYSILIDGSGSAFISITDLOGRDGLTV 61
DB 272 LYQMSVSEAAPGSEVGRVAKADPDIGENGLVTYNIIVDGGMESFELTDTYETQSGVTKL 331

QY 62 RKPLDFESQSRYSFRVEATNTLIDPAYLRGPFKCVASVAVQADAPPPAFQAAHYHL 121
DB 332 KKPVDFFETERYASLKVEAAVNHIDPKFISNGPFKDTVTVKISVEDDEPMPFLAPSYIHE 391
QY 122 VPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIOEEGTIHTAPLDREAR 181
DB 392 VQENAAAGTVGRVHADPDPAANSPIRYSIDRHTDLDREFTINPDGFIKTTKPLDREFT 451
QY 182 AMNLTIVLATEL 193
DB 452 AMNLTIVFAAEI 463

RESULT 8
US-08-738-349-2
Sequence 2, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Eggon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match 53.7%; Score 532; DB 2; Length 796;
Best Local Similarity 50.8%; Pred. No. 1,2e-52;
Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLVGRRLAOPDDGDNALMAYSILIDGSGSAFISITDLOGRDGLTV 60
DB 271 SVYQMSVSEAAPGSEVGRVAKADPDIGENGLVTYNIIVDGDGELPEFTITDTYETQSGVTK 330
QY 61 VRKPLDFESQSRYSFRVEATNTLIDPAYLRGPFKCVASVAVQADAPPPAFQAAHYHL 120

Db 331 LKXVDEFTKAYSLKLEAAVNHIDPFKISNGPFKDVTKISVEDADEPFMLAPSYIH 390
Qy 121 TVPENKAPGLTVGQISADLDSPPSPIRYSILPHSDPERCFSTOPEEGTHTAPLDREA 180
Db 391 EVQENAAAGTVGVRHAKDPDPAANSPIRYSIDRHTDLRFTINPEDGFIKTKKPLDREB 450
Qy 181 RAMNLTVALTEL 193
Db 451 TAWNINISITATEI 463

RESULT 9
US-08-188-228-44
; Sequence 44, Application US/08188228
; Patent No. 5597725

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 52.7%; Score 522; DB 1; Length 532;
Best Local Similarity 49.7%; Pred. No. 9.2e-52;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

Qy 1 SLVQFSVETAGPGLTVGRRAODPDLDGNALMAYSLIDGSGSAFSTIDLGSDLLT 60
Db 279 SLHRSVPEDEVVLGTAIGRVKANDODIGENAOSSYDIIDGDTALFEITSDAQADGVIR 338
Qy 61 VRKPLDFESQSRYSFRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
Db 339 LRKPLDFETKSKYTLKVEAANIHIIDPRFSGRPFKDTATVKIIVEDADEPVSPTYLL 398
Qy 121 TVPENKAPGLTVGQISADLDSPPSPIRYSILPHSDPERCFSTOPEEGTHTAPLDREA 180

Db 399 EVHENAALNSVIGQYARDPDITSSPIRFSIDRHTDLERQFNADDKITLATELDREL 458
Qy 181 RAMNLTVALTEL 193
Db 459 SWNHNISITATEI 471

RESULT 10
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 52.7%; Score 522; DB 1; Length 532;
Best Local Similarity 49.7%; Pred. No. 9.2e-52;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

Qy 1 SLVQFSVETAGPGLTVGRRAODPDLDGNALMAYSLIDGSGSAFSTIDLGSDLLT 60
Db 279 SLHRSVPEDEVVLGTAIGRVKANDODIGENAOSSYDIIDGDTALFEITSDAQADGVIR 338
Qy 61 VRKPLDFESQSRYSFRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
Db 339 LRKPLDFETKSKYTLKVEAANIHIIDPRFSGRPFKDTATVKIIVEDADEPVSPTYLL 398
Qy 121 TVPENKAPGLTVGQISADLDSPPSPIRYSILPHSDPERCFSTOPEEGTHTAPLDREA 180
Db 399 EVHENAALNSVIGQYARDPDITSSPIRFSIDRHTDLERQFNADDKITLATELDREL 458
Qy 181 RAMNLTVALTEL 193
Db 459 SWNHNISITATEI 471

RESULT 11
US-08-188-228-42
; Sequence 42, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-42

Query Match 52.7%; Score 522; DB 1; Length 799;
Best Local Similarity 49.7%; Pred. No. 1.7e-51;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAOPDPLGDNALMAYSLIDGSGSEAFSISTDLQGRDGLLT 60
DB 279 SLVHFSVPEDVLTGTAIGRVKANDQDIGENHQSSTYDIIDGDTALFEITSDAQAGQVIR 338
QY 61 VRKPLDEFSQSYSFREVEATNTLLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
DB 339 LRKPLDEFTKSKYTLKVEANINIHDPFSGRGPKDTATVKIYVEDADEPPVFSPTYLL 398
QY 121 TVPENKAPGTLVQGISAADLDSPASPTRYSLPHSDPERGCSIQPEEGTHTAAPLDREA 180
DB 399 EVHENALNSVIGQVTAARDPDITSSPIRFSIDRHITDERQFINADGKITLATPLDREL 458
QY 181 RAMNLTVLATL 193
DB 459 SVMNHSIATETI 471

RESULT 12
US-08-332-638-42
; Sequence 42, Application US/08332638
; Patent No. 5646250

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 52.7%; Score 522; DB 1; Length 799;
Best Local Similarity 49.7%; Pred. No. 1.7e-51;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAOPDPLGDNALMAYSLIDGSGSEAFSISTDLQGRDGLLT 60
DB 279 SLVHFSVPEDVLTGTAIGRVKANDQDIGENHQSSTYDIIDGDTALFEITSDAQAGQVIR 338
QY 61 VRKPLDEFSQSYSFREVEATNTLLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
DB 339 LRKPLDEFTKSKYTLKVEANINIHDPFSGRGPKDTATVKIYVEDADEPPVFSPTYLL 398
QY 121 TVPENKAPGTLVQGISAADLDSPASPTRYSLPHSDPERGCSIQPEEGTHTAAPLDREA 180
DB 399 EVHENALNSVIGQVTAARDPDITSSPIRFSIDRHITDERQFINADGKITLATPLDREL 458
QY 181 RAMNLTVLATL 193
DB 459 SVMNHSIATETI 471

RESULT 13
US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &


```

; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 559725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-189-228-54

Query Match 52.6%; Score 521; DB 1; Length 793;
Best Local Similarity 49.7%; Pred. No. 2.2e-51;
Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDDPLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLT 60
DB 272 SLVHFSVPEDEVVLGTAIGRVKANDQDIGNAQSSYDIIDGDTALFEITSDAQADGIR 331
QY 61 VRKPLDFESQSSYSFRVATNTLIDPAYLRGPFKDVASVRANQDAPEPPAFQAAYHL 120
DB 332 LRKPLDFETKSKSYTLKDEANVHIDPRSGRPFKDTATVKTIVEDADEPPVSSPTVLL 391
QY 121 TVPENKAPGLVGOISAAIDLSAPSPIRYSILPHSDPERCFISIQEEGTHTAAPLDREA 180
DB 392 EVHENAALNSVIGQVTARPDITSSPIRFSIDRHTDLERQFNINADQKITLATPLDREL 451
QY 181 RAMHNLTVLATEL 193
DB 452 SVMHNTIITATEI 464

RESULT 14
US-08-332-643-48
; Sequence 48, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
```

```

; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-643-48

Query Match 52.6%; Score 521; DB 1; Length 793;
Best Local Similarity 49.7%; Pred. No. 2.2e-51;
Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDDPLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLT 60
DB 272 SLVHFSVPEDEVVLGTAIGRVKANDQDIGNAQSSYDIIDGDTALFEITSDAQADGIR 331
QY 61 VRKPLDFESQSSYSFRVATNTLIDPAYLRGPFKDVASVRANQDAPEPPAFQAAYHL 120
DB 332 LRKPLDFETKSKSYTLKDEANVHIDPRSGRPFKDTATVKTIVEDADEPPVSSPTVLL 391
QY 121 TVPENKAPGLVGOISAAIDLSAPSPIRYSILPHSDPERCFISIQEEGTHTAAPLDREA 180
DB 392 EVHENAALNSVIGQVTARPDITSSPIRFSIDRHTDLERQFNINADQKITLATPLDREL 451
QY 181 RAMHNLTVLATEL 193
DB 452 SVMHNTIITATEI 464

RESULT 15
US-08-332-638-54
; Sequence 54, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 53.6%; Score 521; DB 1; Length 793;

Best Local Similarity 49.7%; Pred. No. 2.2e-51; Mismatches 56; Indels 0; Gaps 0;

Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

Qy	1	SLYQSVETAGPCTLVGRRAODPDLDGNALMAYSLDGESEAFSISTDLQGRDGLT	60
Db	272	SLYHFSYEDVYLGTAIGRVANDQDIGNAQSSYDIIDGDTALFEITSDAQAGDGI	331
Qy	61	VRKPLDPESQSSYFRVEATNTLIDPAYLRGPFKDVASRVAVQDAPEPPAFTQA	120
Db	332	LKRLDPEYTKKSYTLKDEANVHIDPRFSGRGPPKDTATVAKIVEDADEPPVFS	391
Qy	121	TPENKAPGTLVQGISADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAPLD	180
Db	392	EVHENAALNSVIGVTAARDPITSSPIRFSIDRHTDLERQFNINADDKITLATP	451
Qy	181	PAWNLTVLATEL	193
Db	452	SVWNHTITLATEI	464

Search completed: December 8, 2004, 10:01:15
Job time : 24.0142 secs